Single Nucleotide Polymorphisms as Predictive Diagnostics for Adverse Drug Reactions (ADR) and Drug Efficacy

Technical Field

This invention relates to genetic polymorphisms useful for assessing the response to lipid lowering drug therapy and adverse drug reactions of those medicaments. In addition it relates to genetic polymorphisms useful for assessing cardiovascular risks in humans, including, but not limited to, atherosclerosis, ischemia/reperfusion, hypertension, restenosis, arterial inflammation, myocardial infarction, and stroke. Specifically, the present invention identifies and describes gene variations which are individually present in humans with cardiovascular disease states, relative to humans with normal, or non-cardiovascular disease states, and/or in response to medications relevant to cardiovascular disease. Further, the present invention provides methods for the identification and therapeutic use of compounds as treatments of cardiovascular disease or as prophylactic therapy for cardiovascular diseases. Moreover, the present invention provides methods for the diagnostic monitoring of patients undergoing clinical evaluation for the treatment of cardiovascular disease, and for monitoring the efficacy of compounds in clinical trials. Still further, the present invention provides methods to use gene variations to predict personal medication schemes omitting adverse drug reactions and allowing an adjustment of the drug dose to achieve maximum benefit for the patient. Additionally, the present invention describes methods for the diagnostic evaluation and prognosis of various cardiovascular diseases, and for the identification of subjects exhibiting a predisposition to such conditions.

Background of the Invention

Cardiovascular disease is a major health risk throughout the industrialized world.

Cardiovascular diseases include but are not limited by the following disorders of the heart and the vascular system: congestive heart failure, myocardial infarction,

atherosclerosis, ischemic diseases of the heart, coronary heart disease, all kinds of atrial and ventricular arrhythmias, hypertensive vascular diseases and peripheral vascular diseases.

Heart failure is defined as a pathophysiologic state in which an abnormality of cardiac function is responsible for the failure of the heart to pump blood at a rate commensurate with the requirement of the metabolizing tissue. It includes all forms of pumping failure such as high-output and low-output, acute and chronic, right-sided or left-sided, systolic or diastolic, independent of the underlying cause.

Myocardial infarction (MI) is generally caused by an abrupt decrease in coronary blood flow that follows a thrombotic occlusion of a coronary artery previously narrowed by arteriosclerosis. MI prophylaxis (primary and secondary prevention) is included as well as the acute treatment of MI and the prevention of complications.

Ischemic diseases are conditions in which the coronary flow is restricted resulting in an perfusion which is inadequate to meet the myocardial requirement for oxygen. This group of diseases include stable angina, unstable angina and asymptomatic ischemia.

Arrhythmias include all forms of atrial and ventricular tachyarrhythmias (atrial tachycardia, atrial flutter, atrial fibrillation, atrio-ventricular reentrant tachycardia, preexitation syndrome, ventricular tachycardia, ventricular flutter, ventricular fibrillation) as well as bradycardic forms of arrhythmias.

Hypertensive vascular diseases include primary as well as all kinds of secondary arterial hypertension (renal, endocrine, neurogenic, others).

Peripheral vascular diseases are defined as vascular diseases in which arterial and/or venous flow is reduced resulting in an imbalance between blood supply and tissue oxygen demand. It includes chronic peripheral arterial occlusive disease (PAOD),

acute arterial thrombosis and embolism, inflammatory vascular disorders, Raynaud's phenomenon and venous disorders.

Atherosclerosis, the most prevalent of vascular diseases, is the principal cause of heart attack, stroke, and gangrene of the extremities, and thereby the principal cause of death. Atherosclerosis is a complex disease involving many cell types and molecular factors (for a detailed review, see Ross, 1993, Nature 362: 801-809 and Lusis, A. J., Nature 407, 233-241 (2000)). The process, in normal circumstances a protective response to insults to the endothelium and smooth muscle cells (SMCs) of the wall of the artery, consists of the formation of fibrofatty and fibrous lesions or plaques, preceded and accompanied by inflammation. The advanced lesions of atherosclerosis may occlude the artery concerned, and result from an excessive inflammatory-fibroproliferative response to numerous different forms of insult. For example, shear stresses are thought to be responsible for the frequent occurrence of atherosclerotic plaques in regions of the circulatory system where turbulent blood flow occurs, such as branch points and irregular structures.

The first observable event in the formation of an atherosclerotic plaque occurs when blood-borne monocytes adhere to the vascular endothelial layer and transmigrate through to the sub-endothelial space. Adjacent endothelial cells at the same time produce oxidized low density lipoprotein (LDL). These oxidized LDLs are then taken up in large amounts by the monocytes through scavenger receptors expressed on their surfaces. In contrast to the regulated pathway by which native LDL (nLDL) is taken up by nLDL specific receptors, the scavenger pathway of uptake is not regulated by the monocytes.

These lipid-filled monocytes are called foam cells, and are the major constituent of the fatty streak. Interactions between foam cells and the endothelial and SMCs which surround them lead to a state of chronic local inflammation which can eventually lead to smooth muscle cell proliferation and migration, and the formation of a fibrous

plaque. Such plaques occlude the blood vessel concerned and thus restrict the flow of blood, resulting in ischemia.

Ischemia is a condition characterized by a lack of oxygen supply in tissues of organs due to inadequate perfusion. Such inadequate perfusion can have number of natural causes, including atherosclerotic or restenotic lesions, anemia, or stroke, to name a few. Many medical interventions, such as the interruption of the flow of blood during bypass surgery, for example, also lead to ischemia. In addition to sometimes being caused by diseased cardiovascular tissue, ischemia may sometimes affect cardiovascular tissue, such as in ischemic heart disease. Ischemia may occur in any organ, however, that is suffering a lack of oxygen supply.

The most common cause of ischemia in the heart is atherosclerotic disease of epicardial coronary arteries. By reducing the lumen of these vessels, atherosclerosis causes an absolute decrease in myocardial perfusion in the basal state or limits appropriate increases in perfusion when the demand for flow is augmented. Coronary blood flow can also be limited by arterial thrombi, spasm, and, rarely, coronary emboli, as well as by ostial narrowing due to luetic aortitis. Congenital abnormalities, such as anomalous origin of the left anterior descending coronary artery from the pulmonary artery, may cause myocardial ischemia and infarction in infancy, but this cause is very rare in adults. Myocardial ischemia can also occur if myocardial oxygen demands are abnormally increased, as in severe ventricular hypertrophy due to hypertension or aortic stenosis. The latter can be present with angina that is indistinguishable from that caused by coronary atherosclerosis. A reduction in the oxygen-carrying capacity of the blood, as in extremely severe anemia or in the presence of carboxy-hemoglobin, is a rare cause of myocardial ischemia. Not infrequently, two or more causes of ischemia will coexist, such as an increase in oxygen demand due to left ventricular hypertrophy and a reduction in oxygen supply secondary to coronary atherosclerosis.

The foregoing studies are aimed at defining the role of particular gene variations presumed to be involved in the misleading of normal cellular function leading to cardiovascular disease. However, such approaches cannot identify the full panoply of gene variations that are involved in the disease process.

At present, the only available treatments for cardiovascular disorders are pharmaceutical based medications that are not targeted to an individual‘s actual defect; examples include angiotensin converting enzyme (ACE) inhibitors and diuretics for hypertension, insulin supplementation for non-insulin dependent diabetes mellitus (NIDDM), cholesterol reduction strategies for dyslipidaemia, anticoagulants, β blockers for cardiovascular disorders and weight reduction strategies for obesity. If targeted treatment strategies were available it might be possible to predict the response to a particular regime of therapy and could markedly increase the effectiveness of such treatment. Although targeted therapy requires accurate diagnostic tests for disease susceptibility, once these tests are developed the opportunity to utilize targeted therapy will become widespread. Such diagnostic tests could initially serve to identify individuals at most risk of hypertension and could allow them to make changes in lifestyle or diet that would serve as preventative measures. The benefits associated by coupling the diagnostic tests with a system of targeted therapy could include the reduction in dosage of administered drugs and thus the amount of unpleasant side effects suffered by an individual. In more severe cases a diagnostic test may suggest that earlier surgical intervention would be useful in preventing a further deterioration in condition.

It is an object of the invention to provide genetic diagnosis of predisposition or susceptibility for cardiovascular diseases. Another related object is to provide treatment to reduce or prevent or delay the onset of disease in those predisposed or susceptible to this disease. A further object is to provide means for carrying out this diagnosis.

Accordingly, a first aspect of the invention provides a method of diagnosis of disease in an individual, said method comprising determining one, various or all genotypes in said individual of the genes listed in the Examples.

In another aspect, the invention provides a method of identifying an individual predisposed or susceptible to a disease, said method comprising determining one, various or all genotypes in said individual of the genes listed in the Examples.

The invention is of advantage in that it enables diagnosis of a disease or of certain disease states via genetic analysis which can yield useable results before onset of disease symptoms, or before onset of severe symptoms. The invention is further of advantage in that it enables diagnosis of predisposition or susceptibility to a disease or of certain disease states via genetic analysis.

The invention may also be of use in confirming or corroborating the results of other diagnostic methods. The diagnosis of the invention may thus suitably be used either as an isolated technique or in combination with other methods and apparatus for diagnosis, in which latter case the invention provides a further test on which a diagnosis may be assessed.

The present invention stems from using allelic association as a method for genotyping individuals; allowing the investigation of the molecular genetic basis for cardiovascular diseases. In a specific embodiment the invention tests for the polymorphisms in the sequences of the listed genes in the Examples. The invention demonstrates a link between this polymorphisms and predispositions to cardio-vascular diseases by showing that allele frequencies significantly differ when individuals with "bad" serum lipids are compared to individuals with "good" serum levels. The meaning of "good and bad" serum lipid levels is defined in Table 1a.

Certain disease states would benefit, that is to say the suffering of the patient may be reduced or prevented or delayed, by administration of treatment or therapy in

advance of disease appearance; this can be more reliably carried out if advance diagnosis of predisposition or susceptibility to disease can be diagnosed.

Pharmacogenomics and adverse drug reactions

Adverse drug reactions (ADRs) remain a major clinical problem. A recent meta-analysis suggested that in the USA in 1994, ADRs were responsible for 100 000 deaths, making them between the fourth and sixth commonest cause of death (Lazarou 1998,. J. Am. Med. Assoc. 279:1200). Although these figures have been heavily criticized, they emphasize the importance of ADRs. Indeed, there is good evidence that ADRs account for 5% of all hospital admissions and increase the length of stay in hospital by two days at an increased cost of ~$2500 per patient. ADRs are also one of the commonest causes of drug withdrawal, which has enormous financial implications for the pharmaceutical industry. ADRs, perhaps fortunately, only affect a minority of those taking a particular drug. Although factors that determine susceptibility are unclear in most cases, there is increasing interest in the role of genetic factors. Indeed, the role of inheritable variations in predisposing patients to ADRs has been appreciated since the late 1950s and early 1960s through the discovery of deficiencies in enzymes such as pseudocholinesterase (butyryl-cholinesterase) and glucose-6-phosphate dehydrogenase (G6PD). More recently, with the first draft of the human genome just completed, there has been renewed interest in this area with the introduction of terms such as pharmacogenomics and toxicogenomics . Essentially, the aim of pharmacogenomics and pharmacogenetics is to produce personalized medicines, whereby administration of the drug class and dosage is tailored to an individual genotype. Thus, the term pharmacogenetics embraces both efficacy and toxicity.

The 3-hydroxy-3-methylglutaryl coenzyme A (HMG-CoA) reductase inhibitors ("statins") specifically inhibit the enzyme HMG-CoA reductase which catalyzes the rate limiting step in cholesterol biosynthesis. These drugs are effective in reducing the primary and secondary risk of coronary artery disease and coronary events, such

as heart attack, in middle-aged and older men and women, in both diabetic and non-diabetic patients, and are often prescribed for patients with hyperlipidemia. Statins used in secondary prevention of coronary artery or heart disease significantly reduce the risk of stroke, total mortality and morbidity and attacks of myocardial ischemia; the use of statins is also associated with improvements in endothelial and fibrinolytic functions and decreased platelet thrombus formation.

The tolerability of these drugs during long term administration is an important issue. Adverse reactions involving skeletal muscle are not uncommon, and sometimes serious adverse reactions involving skeletal muscle such as myopathy and rhabdomyolysis may occur, requiring discontinuation of the drug. In addition an increase in serum creatine kinase (CK) may be a sign of a statin related adverse event. The extend of such adverse events can be read from the extend of the CK level increase (as compared to the upper limit of normal [ULN]).

Occasionally arthralgia, alone or in association with myalgia, has been reported. Also an elevation of liver transaminases has been associated with statin administration.

It was shown that the drug response to statin therapy is a class effects, i.e. all known and presumably also all so far undiscovered statins share the same benefical and harmful effects (Ucar, M. et al., Drug Safety 2000, 22:441). It follows that the discovery of diagnostic tools to predict the drug response to a single statin will also be of aid to guide therapy with other statins.

The present invention provides diagnostic tests to predict the patient's individual response to statin therapy. Such responses include, but are not limited by the extent of adverse drug reactions, the level of lipid lowering or the drug's influence on disease states. Those diagnostic tests may predict the response to statin therapy either alone or in combination with another diagnostic test or another drug regimen.

Detailed Description of the Invention

The present invention is based at least in part on the discovery that a specific allele of a polymorphic region of a so called "candidate gene" (as defined below) is associated with CVD or drug response.

For the present invention the following candidate genes were analyzed:

- Genes found to be expressed in cardiac tissue (Hwang et al., Circulation 1997, 96:4146-4203).
- Genes from the following metabolic pathways and their regulatory elements:

Lipid metabolism

Numerous studies have shown a connection between serum lipid levels and cardiovascular diseases. Candidate genes falling into this group include but are not limited by genes of the cholesterol pathway, apolipoproteins and their modifiying factors.

Coagulation

Ischemic diseases of the heart and in particular myocardial infarction may be caused by a thrombotic occlusion. Genes falling into this group include all genes of the coagulation cascade and their regulatory elements.

Inflammation

Complications of atherosclerosis are the most common causes of death in Western societies. In broad outline atherosclerosis can be considered to be a form of chronic inflammation resulting from interaction modified lipoproteins, monocyte-derived macrophages,T cells, and the normal cellular elements of the arterial wall. This

inflammatory process can ultimately lead to the development of complex lesions, or plaques, that protrude into the arterial lumen. Finally plaque rupture and thrombosis result in the acute clinical complications of myocardial infarction and stroke (Glass et al., Cell 2001, 104:503-516).

It follows that all genes related to inflammatory processes, including but not limited by cytokines, cytokine receptors and cell adhesion molecules are candidate genes for CVD.

Glucose and energy metabolism

As glucose and energy metabolism is interdependent with the metabolism of lipids (see above) also the former pathways contain candidate genes. Energy metabolism in general also relates to obesity, which is an independent risk factor for CVD (Melanson et al., Cardiol Rev 2001 9:202-207). In addition high blood glucose levels are associated with many microvascular and macrovascular complications and may therefore affect an individuals disposition to CVD (Duckworth, Curr Atheroscler Rep 2001, 3:383-391).

Hypertension

As hypertension is an independent risk factor for CVD, also genes that are involved in the regulation of systolic and diastolic blood pressure affect an individuals risk for CVD (Safar, Curr Opin Cardiol 2000, 15:258-263). Interestingly hypertension and diabetes (see above) appear to be interdependent, since hypertension is approximately twice as frequent in patients with diabetes compared with patients without the disease. Conversely, recent data suggest that hypertensive persons are more predisposed to the development of diabetes than are normotensive persons (Sowers et al., Hypertension 2001, 37:1053-1059).

Genes related to drug response

Those genes include metabolic pathways involved in the absorption, distribution, metabolism, excretion and toxicity (ADMET) of drugs. Prominent members of this group are the cytochrome P450 proteins which catalyze many reactions involved in drug metabolism.

Unclassified genes

As stated above, the mechanisms that lead to cardiovascular diseases or define the patient's individual response to drugs are not completely elucidated. Hence also candidate genes were analysed, which could not be assigned to the above listed categories. The present invention is based at least in part on the discovery of polymorphisms, that lie in genomic regions of unknown physiological function.

Results

After conducting an association study, we surprisingly found polymorphic sites in a number of candidate genes which show a strong correlation with the following phenotypes of the patients analysed: "Healthy" as used herein refers to individuals that neither suffer from existing CVD, nor exhibit an increased risk for CVD through their serum lipid level profile. "CVD prone" as used herein refers to individuals with existing CVD and/or a serum lipid profile that confers a high risk to get CVD (see Table 1a for definitions of healthy and CVD prone serum lipid levels). "High responder" as used herein refers to patients who benefit from relatively small amounts of a given drug. "Low responder" as used herein refers to patients who need relatively high doses in order to obtain benefit from the medication. "Tolerant patient" refers to individuals who can tolerate high doses of a medicament without exhibiting adverse drug reactions. "ADR patient" as used herein refers to individuals who suffer from ADR or show clinical symptoms (like creatine kinase elevation in

blood) even after receiving only minor doses of a medicament (see Table 1b for a detailed definition of drug response phenotypes).

Polymorphic sites in candidate genes that were found to be significantly associated with either of the above mentioned phenotypes will be referred to as "phenotype associated SNPs" (PA SNPs). The respective genomic loci that harbour PA SNPs will be referred to as "phenotype associated genes" (PA genes), irrespective of the actual function of this gene locus.

As PA SNPs are linked to other SNPs in neighboring genes on a chromosome (Linkage Disequilibrium) those SNPs could also be used as marker SNPs. In a recent publication it was shown that SNPs are linked over 100 kb in some cases more than 150 kb (Reich D.E. et al. Nature 411, 199-204, 2001). Hence SNPs lying in regions neighbouring PA SNPs could be linked to the latter and by this being a diagnostic marker. These associations could be performed as described for the gene polymorphism in methods.

Definitions

For convenience, the meaning of certain terms and phrases employed in the specification, examples, and appended claims are provided below. Moreover, the definitions by itself are intended to explain a further background of the invention.

The term "allele", which is used interchangeably herein with "allelic variant" refers to alternative forms of a gene or portions thereof. Alleles occupy the same locus or position on homologous chromosomes. When a subject has two identical alleles of a gene, the subject is said to be homozygous for the gene or allele. When a subject has two different alleles of a gene, the subject is said to be heterozygous for the gene. Alleles of a specific gene can differ from each other in a single nucleotide, or several nucleotides, and can include substitutions, deletions, and insertions of nucleotides. An allele of a gene can also be a form of a gene containing a mutation.

The term "allelic variant of a polymorphic region of a gene" refers to a region of a gene having one of several nucleotide sequences found in that region of the gene in other individuals.

"Homology" or "identity" or "similarity" refers to sequence similarity between two peptides or between two nucleic acid molecules. Homology can be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When a position in the compared sequence is occupied by the same base or amino acid, then the molecules are homologous at that position. A degree of homology between sequences is a function of the number of matching or homologous positions shared by the sequences. An "unrelated" or "non-homologous" sequence shares less than 40% identity, though preferably less than 25% identity, with one of the sequences of the present invention.

The term "a homologue of a nucleic acid" refers to a nucleic acid having a nucleotide sequence having a certain degree of homology with the nucleotide sequence of the nucleic acid or complement thereof. A homologue of a double stranded nucleic acid having SEQ ID NO. X is intended to include nucleic acids having a nucleotide sequence which has a certain degree of homology with SEQ ID NO. X or with the complement thereof. Preferred homologous of nucleic acids are capable of hybridizing to the nucleic acid or complement thereof.

The term "interact" as used herein is meant to include detectable interactions between molecules, such as can be detected using, for example, a hybridization assay.

The term interact is also meant to include "binding" interactions between molecules. Interactions may be, for example, protein-protein, protein-nucleic acid, protein-small molecule or small molecule-nucleic acid in nature.

The term "intronic sequence" or "intronic nucleotide sequence" refers to the nucleotide sequence of an intron or portion thereof.

The term "isolated" as used herein with respect to nucleic acids, such as DNA or RNA, refers to molecules separated from other DNAs or RNAs, respectively, that are present in the natural source of the macromolecule. The term isolated as used herein also refers to a nucleic acid or peptide that is substantially free of cellular material, viral material, or culture medium when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized.

Moreover, an "isolated nucleic acid" is meant to include nucleic acid fragments which are not naturally occurring as fragments and would not be found in the natural state. The term "isolated" is also used herein to refer to polypeptides which are isolated from other cellular proteins and is meant to encompass both purified and recombinant polypeptides.

The term "lipid" shall refer to a fat or fat-like substance that is insoluble in polar solvents such as water. The term "lipid" is intended to include true fats (e.g. esters of fatty acids and glycerol); lipids (phospholipids, cerebrosides, waxes); sterols (cholesterol, ergosterol) and lipoproteins (e.g. HDL, LDL and VLDL).

The term "locus" refers to a specific position in a chromosome. For example, a locus of a gene refers to the chromosomal position of the gene.

The term "modulation" as used herein refers to both up-regulation, (i.e., activation or stimulation), for example by agonizing, and down-regulation (i.e. inhibition or suppression), for example by antagonizing of a bioactivity (e.g. expression of a gene).

The term "molecular structure" of a gene or a portion thereof refers to the structure as defined by the nucleotide content (including deletions, substitutions, additions of one

or more nucleotides), the nucleotide sequence, the state of methylation, and/or any other modification of the gene or portion thereof.

The term "mutated gene" refers to an allelic form of a gene, which is capable of altering the phenotype of a subject having the mutated gene relative to a subject which does not have the mutated gene. If a subject must be homozygous for this mutation to have an altered phenotype, the mutation is said to be recessive. If one copy of the mutated gene is sufficient to alter the genotype of the subject, the mutation is said to be dominant. If a subject has one copy of the mutated gene and has a phenotype that is intermediate between that of a homozygous and that of a heterozygous (for that gene) subject, the mutation is said to be co-dominant.

As used herein, the term "nucleic acid" refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). The term should also be understood to include, as equivalents, derivatives, variants and analogs of either RNA or DNA made from nucleotide analogs, including peptide nucleic acids (PNA), morpholino oligonucleotides (J. Summerton and D. Weller, Antisense and Nucleic Acid Drug Development 7:187 (1997)) and, as applicable to the embodiment being described, single (sense or antisense) and double-stranded polynucleotides. Deoxyribonucleotides include deoxyadenosine, deoxycytidine, deoxyguanosine, and deoxythymidine. For purposes of clarity, when referring herein to a nucleotide of a nucleic acid, which can be DNA or an RNA, the term "adenosine", "cytidine", "guanosine", and "thymidine" are used. It is understood that if the nucleic acid is RNA, a nucleotide having a uracil base is uridine.

The term "nucleotide sequence complementary to the nucleotide sequence set forth in SEQ ID NO. x" refers to the nucleotide sequence of the complementary strand of a nucleic acid strand having SEQ ID NO. x. The term "complementary strand" is used herein interchangeably with the term "complement". The complement of a nucleic acid strand can be the complement of a coding strand or the complement of a non-coding strand. When referring to double stranded nucleic acids, the complement of a

nucleic acid having SEQ ID NO. x refers to the complementary strand of the strand having SEQ ID NO. x or to any nucleic acid having the nucleotide sequence of the complementary strand of SEQ ID NO. x. When referring to a single stranded nucleic acid having the nucleotide sequence SEQ ID NO. x, the complement of this nucleic acid is a nucleic acid having a nucleotide sequence which is complementary to that of SEQ ID NO. x. The nucleotide sequences and complementary sequences thereof are always given in the 5' to 3' direction. The term "complement" and "reverse complement" are used interchangeably herein.

The term "operably linked" is intended to mean that the promoter is associated with the nucleic acid in such a manner as to facilitate transcription of the nucleic acid.

The term "polymorphism" refers to the coexistence of more than one form of a gene or portion thereof. A portion of a gene of which there are at least two different forms, i.e., two different nucleotide sequences, is referred to as a "polymorphic region of a gene". A polymorphic region can be a single nucleotide, the identity of which differs in different alleles. A polymorphic region can also be several nucleotides long.

A "polymorphic gene" refers to a gene having at least one polymorphic region.

To describe a “polymorphic site” in a nucleotide sequence often there is used an “ambiguity code” that stands for the possible variations of nucleotides in one site. The list of ambiguity codes is summarized in the following table:

Ambiguity Codes (IUPAC Nomenclature)	
B	c/g/t
D	a/g/t
H	a/c/t
K	g/t
M	a/c
N	a/c/g/t
R	a/g
S	c/g
V	a/c/g
W	a/t
Y	c/t

So, for example, a "R" in a nucleotide sequence means that either an "a" or a "g" could be at that position.

The terms "protein", "polypeptide" and "peptide" are used interchangeably herein when referring to a gene product.

A "regulatory element", also termed herein "regulatory sequence is intended to include elements which are capable of modulating transcription from a basic promoter and include elements such as enhancers and silencers. The term "enhancer", also referred to herein as "enhancer element", is intended to include regulatory elements capable of increasing, stimulating, or enhancing transcription from a basic promoter. The term "silencer", also referred to herein as "silencer element" is intended to include regulatory elements capable of decreasing, inhibiting, or repressing transcription from a basic promoter. Regulatory elements are typically present in 5' flanking regions of genes. However, regulatory elements have also been shown to be present in other regions of a gene, in particular in introns. Thus, it is possible that genes have regulatory elements located in introns, exons, coding

regions, and 3' flanking sequences. Such regulatory elements are also intended to be encompassed by the present invention and can be identified by any of the assays that can be used to identify regulatory elements in 5' flanking regions of genes.

The term "regulatory element" further encompasses "tissue specific" regulatory elements, i.e., regulatory elements which effect expression of the selected DNA sequence preferentially in specific cells (e.g., cells of a specific tissue). gene expression occurs preferentially in a specific cell if expression in this cell type is significantly higher than expression in other cell types. The term "regulatory element" also encompasses non-tissue specific regulatory elements, i.e., regulatory elements which are active in most cell types. Furthermore, a regulatory element can be a constitutive regulatory element, i.e., a regulatory element which constitutively regulates transcription, as opposed to a regulatory element which is inducible, i.e., a regulatory element which is active primarily in response to a stimulus. A stimulus can be, e.g., a molecule, such as a hormone, cytokine, heavy metal, phorbol ester, cyclic AMP (cAMP), or retinoic acid.

Regulatory elements are typically bound by proteins, e.g., transcription factors. The term "transcription factor" is intended to include proteins or modified forms thereof, which interact preferentially with specific nucleic acid sequences, i.e., regulatory elements, and which in appropriate conditions stimulate or repress transcription. Some transcription factors are active when they are in the form of a monomer. Alternatively, other transcription factors are active in the form of a dimer consisting of two identical proteins or different proteins (heterodimer). Modified forms of transcription factors are intended to refer to transcription factors having a post-translational modification, such as the attachment of a phosphate group. The activity of a transcription factor is frequently modulated by a post-translational modification. For example, certain transcription factors are active only if they are phosphorylated on specific residues. Alternatively, transcription factors can be active in the absence of phosphorylated residues and become inactivated by phosphorylation. A list of

known transcription factors and their DNA binding site can be found, e.g., in public databases, e.g., TFMATRIX Transcription Factor Binding Site Profile database.

As used herein, the term "specifically hybridizes" or "specifically detects" refers to the ability of a nucleic acid molecule of the invention to hybridize to at least approximately 6, 12, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130 or 140 consecutive nucleotides of either strand of a gene.

The term "wild-type allele" refers to an allele of a gene which, when present in two copies in a subject results in a wild-type phenotype. There can be several different wild-type alleles of a specific gene, since certain nucleotide changes in a gene may not affect the phenotype of a subject having two copies of the gene with the nucleotide changes.

"Adverse drug reaction" (ADR) as used herein refers to an appreciably harmful or unpleasant reaction, resulting from an intervention related to the use of a medicinal product, whichpredicts hazard from future administration and warrants prevention or specific treatment, or alteration of the dosage regimen, or withdrawal of the product. In it's most severe form an ADR might lead to the death of an individual.

The term "Drug Response" is intended to mean any response that a patient exhibits upon drug administration. Specifically drug response includes beneficial, i.e. desired drug effects, ADR or no detectable reaction at all. More specifically the term drug response could also have a qualitative meaning, i.e. it embraces low or high beneficial effects, respectively and mild or severe ADR, respectively. The term "Statin Response" as used herein refers to drug response after statin administration. An individual drug response includes also a good or bad metabolizing of the drug, meaning that "bad metabolizers" accumulate the drug in the body and by this could show side effects of the drug due to accumulative overdoses.

"Candidate gene" as used herein includes genes that can be assigned to either normal cardiovascular function or to metabolic pathways that are related to onset and/or progression of cardiovascular diseases.

With regard to drug response the term "candidate gene" includes genes that can be assigned to distinct phenotypes regarding the patient's response to drug administration. Those phenotypes may include patients who benefit from relatively small amounts of a given drug (high responders) or patients who need relatively high doses in order to obtain the same benefit (low responders). In addition those phenotypes may include patients who can tolerate high doses of a medicament without exhibiting ADR, or patients who suffer from ADR even after receiving only low doses of a medicament.

As neither the development of cardiovascular diseases nor the patient's response to drug administration is completely understood, the term "candidate gene" may also comprise genes with presently unknown function.

"PA SNP" (phenotype associated SNP) refers to a polymorphic site which shows a significant association with a patients phenotype (healthy, diseased, low or high responder, drug tolerant, ADR prone, etc.)

"PA gene" (phenotype associated gene) refers to a genomic locus harbouring a PA SNP, irrespective of the actual function of this gene locus.

PA gene polypeptide refers to a polypeptide encoded at least in part by a PA gene.

The term “Secondary SNP” is intended to mean a SNP that is in neighborhood to at least one other (“primary”) SNP. Due to linkage disequillibrium both primary and secondary SNP(s) might shown a similar association with a phenotype.

The term "Haplotype" as used herein refers to a group of two or more SNPs that are functionally and/or spatially linked. I.e. haplotypes define groups of SNPs that lie inside genes belonging to identical (or related metabolic) pathways and/or lie on the same chromosome. Haplotypes are expected to give better predictive/diagnostic information than a single SNP

The term "statin" is intended to embrace all inhibitors of the enzyme 3-hydroxy-3-methylglutaryl coenzyme A (HMG-CoA) reductase. Statins specifically inhibit the enzyme HMG-CoA reductase which catalyzes the rate limiting step in cholesterol biosynthesis. Known statins are Atorvastatin, Cerivastatin, Fluvastatin, Lovastatin, Pravastatin and Simvastatin.

Methods for Assessing Cardiovascular Status

The present invention provides diagnostic methods for assessing cardiovascular status in a human individual. Cardiovascular status as used herein refers to the physiological status of an individual's cardiovascular system as reflected in one or more markers or indicators. Status markers include without limitation clinical measurements such as, e.g., blood pressure, electrocardiographic profile, and differentiated blood flow analysis as well as measurements of LDL- and HDL-Cholesterol levels, other lipids and other well established clinical parameters that are standard in the art. Status markers according to the invention include diagnoses of one or more cardiovascular syndromes, such as, e.g., hypertension, acute myocardial infarction, silent myocardial infarction, stroke, and atherosclerosis. It will be understood that a diagnosis of a cardiovascular syndrome made by a medical practitioner encompasses clinical measurements and medical judgement. Status markers according to the invention are assessed using conventional methods well known in the art. Also included in the evaluation of cardiovascular status are quantitative or qualitative changes in status markers with time, such as would be used, e.g., in the determination of an individual's response to a particular therapeutic regimen.

The methods are carried out by the steps of:

(i) determining the sequence of one or more polymorphic positions within one, several or all of the genes listed in Examples or other genes mentioned in this file in the individual to establish a polymorphic pattern for the individual; and

(ii) comparing the polymorphic pattern established in (i) with the polymorphic patterns of humans exhibiting different markers of cardiovascular status. The polymorphic pattern of the individual is, preferably, highly similar and, most preferably, identical to the polymorphic pattern of individuals who exhibit particular status markers, cardiovascular syndromes, and/or particular patterns of response to therapeutic interventions. Polymorphic patterns may also include polymorphic positions in other genes which are shown, in combination with one or more polymorphic positions in the genes listed in the Examples, to correlate with the presence of particular status markers. In one embodiment, the method involves comparing an individual's polymorphic pattern with polymorphic patterns of individuals who have been shown to respond positively or negatively to a particular therapeutic regimen. Therapeutic regimen as used herein refers to treatments aimed at the elimination or amelioration of symptoms and events associated cardiovascular disease. Such treatments include without limitation one or more of alteration in diet, lifestyle, and exercise regimen; invasive and noninvasive surgical techniques such as atherectomy, angioplasty, and coronary bypass surgery; and pharmaceutical interventions, such as administration of ACE inhibitors, angiotensin II receptor antagonists, diuretics, alpha-adrenoreceptor antagonists, cardiac glycosides, phosphodiesterase inhibitors, beta-adrenoreceptor antagonists, calcium channel blockers, HMG-CoA reductase inhibitors, imidazoline receptor blockers, endothelin receptor blockers, organic nitrites, and modulators of protein function of genes listed in the Examples. Interventions with pharmaceutical agents not yet known whose activity

correlates with particular polymorphic patterns associated with cardiovascular disease are also encompassed. It is contemplated, for example, that patients who are candidates for a particular therapeutic regimen will be screened for polymorphic patterns that correlate with responsivity to that particular regimen.

In a preferred embodiment, the method involves comparing an individual's polymorphic pattern with polymorphic patterns of individuals who exhibit or have exhibited one or more markers of cardiovascular disease, such as, e.g., elevated LDL-Cholesterol levels, high blood pressure, abnormal electrocardiographic profile, myocardial infarction, stroke, or atherosclerosis.

In another embodiment, the method involves comparing an individual's polymorphic pattern with polymorphic patterns of individuals who exhibit or have exhibited one or more drug related phenotypes, such as, e.g., low or high drug response, or adverse drug reactions.

In practicing the methods of the invention, an individual's polymorphic pattern can be established by obtaining DNA from the individual and determining the sequence at predetermined polymorphic positions in the genes such as those described in this file.

The DNA may be obtained from any cell source. Non-limiting examples of cell sources available in clinical practice include blood cells, buccal cells, cervicovaginal cells, epithelial cells from urine, fetal cells, or any cells present in tissue obtained by biopsy. Cells may also be obtained from body fluids, including without limitation blood, saliva, sweat, urine, cerebrospinal fluid, feces, and tissue exudates at the site of infection or inflammation. DNA is extracted from the cell source or body fluid using any of the numerous methods that are standard in the art. It will be understood that the particular method used to extract DNA will depend on the nature of the source.

Diagnostic and Prognostic Assays

The present invention provides methods for determining the molecular structure of at least one polymorphic region of a gene, specific allelic variants of said polymorphic region being associated with cardiovascular disease. In one embodiment, determining the molecular structure of a polymorphic region of a gene comprises determining the identity of the allelic variant. A polymorphic region of a gene, of which specific alleles are associated with cardiovascular disease can be located in an exon, an intron, at an intron/exon border, or in the promoter of the gene.

The invention provides methods for determining whether a subject has, or is at risk, of developing a cardiovascular disease. Such disorders can be associated with an aberrant gene activity, e.g., abnormal binding to a form of a lipid, or an aberrant gene protein level. An aberrant gene protein level can result from an aberrant transcription or post-transcriptional regulation. Thus, allelic differences in specific regions of a gene can result in differences of gene protein due to differences in regulation of expression. In particular, some of the identified polymorphisms in the human gene may be associated with differences in the level of transcription, RNA maturation, splicing, or translation of the gene or transcription product.

In preferred embodiments, the methods of the invention can be characterized as comprising detecting, in a sample of cells from the subject, the presence or absence of a specific allelic variant of one or more polymorphic regions of a gene. The allelic differences can be: (i) a difference in the identity of at least one nucleotide or (ii) a difference in the number of nucleotides, which difference can be a single nucleotide or several nucleotides.

A preferred detection method is allele specific hybridization using probes overlapping the polymorphic site and having about 5, 10, 20, 25, or 30 nucleotides around the polymorphic region. Examples of probes for detecting specific allelic

variants of the polymorphic region located in intron X are probes comprising a nucleotide sequence set forth in any of SEQ ID NO. X. In a preferred embodiment of the invention, several probes capable of hybridizing specifically to allelic variants are attached to a solid phase support, e.g., a "chip". Oligonucleotides can be bound to a solid support by a variety of processes, including lithography. For example a chip can hold up to 250,000 oligonucleotides (GeneChip, Affymetrix). Mutation detection analysis using these chips comprising oligonucleotides, also termed "DNA probe arrays" is described e.g., in Cronin et al. (1996) Human Mutation 7:244 and in Kozal et al. (1996) Nature Medicine 2:753. In one embodiment, a chip comprises all the allelic variants of at least one polymorphic region of a gene. The solid phase support is then contacted with a test nucleic acid and hybridization to the specific probes is detected. Accordingly, the identity of numerous allelic variants of one or more genes can be identified in a simple hybridization experiment. For example, the identity of the allelic variant of the nucleotide polymorphism of nucleotide A or G at position 33 of Seq ID 1 (baySNP179) and that of other possible polymorphic regions can be determined in a single hybridization experiment.

In other detection methods, it is necessary to first amplify at least a portion of a gene prior to identifying the allelic variant. Amplification can be performed, e.g., by PCR and/or LCR, according to methods known in the art. In one embodiment, genomic DNA of a cell is exposed to two PCR primers and amplification for a number of cycles sufficient to produce the required amount of amplified DNA. In preferred embodiments, the primers are located between 40 and 350 base pairs apart. Preferred primers for amplifying gene fragments of genes of this file are listed in Table 2 in the Examples.

Alternative amplification methods include: self sustained sequence replication (Guatelli, J. C. et al., 1990, Proc. Natl. Acad. Sci. U.S.A. 87:1874-1878), transcriptional amplification system (Kwoh, D. Y. et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:1173-1177), Q-Beta Replicase (Lizardi, P. M. et al., 1988, Bio/Technology 6:1197), or any other nucleic acid amplification method, followed

by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In one embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence at least a portion of a gene and detect allelic variants, e.g., mutations, by comparing the sequence of the sample sequence with the corresponding wild-type (control) sequence. Exemplary sequencing reactions include those based on techniques developed by Maxam and Gilbert (Proc. Natl Acad Sci USA (1977) 74:560) or Sanger (Sanger et al (1977) Proc. Nat. Acad. Sci 74:5463). It is also contemplated that any of a variety of automated sequencing procedures may be utilized when performing the subject assays (Biotechniques (1995) 19:448), including sequencing by mass spectrometry (see, for example, U.S. Pat. No. 5,547,835 and international patent application Publication Number WO 94/16101, entitled DNA Sequencing by Mass Spectrometry by H. Koster; U.S. Pat. No. 5,547,835 and international patent application Publication Number WO 94/21822 entitled "DNA Sequencing by Mass Spectrometry Via Exonuclease Degradation" by H. Koster), and U.S. Pat. No. 5,605,798 and International Patent Application No. PCT/US96/03651 entitled DNA Diagnostics Based on Mass Spectrometry by H. Koster; Cohen et al. (1996) Adv Chromatogr 36:127-162; and Griffin et al. (1993) Appl Biochem Biotechnol 38:147-159). It will be evident to one skilled in the art that, for certain embodiments, the occurrence of only one, two or three of the nucleic acid bases need be determined in the sequencing reaction. For instance, A-track or the like, e.g., where only one nucleotide is detected, can be carried out.

Yet other sequencing methods are disclosed, e.g., in U.S. Pat. No. 5,580,732 entitled "Method of DNA sequencing employing a mixed DNA-polymer chain probe" and U.S. Pat. No. 5,571,676 entitled "Method for mismatch-directed in vitro DNA sequencing".

In some cases, the presence of a specific allele of a gene in DNA from a subject can be shown by restriction enzyme analysis. For example, a specific nucleotide polymorphism can result in a nucleotide sequence comprising a restriction site which is absent from the nucleotide sequence of another allelic variant.

In other embodiments, alterations in electrophoretic mobility is used to identify the type of gene allelic variant. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita et al. (1989) Proc Natl. Acad. Sci USA 86:2766, see also Cotton (1993) Mutat Res 285:125-144; and Hayashi (1992) Genet Anal Tech Appl 9:73-79). Single-stranded DNA fragments of sample and control nucleic acids are denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In another preferred embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (Keen et al. (1991) Trends Genet 7:5).

In yet another embodiment, the identity of an allelic variant of a polymorphic region is obtained by analyzing the movement of a nucleic acid comprising the polymorphic region in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE) (Myers et al (1985) Nature 313:495). When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing agent gradient to identify differences in the mobility of control and sample DNA (Rosenbaum and Reissner (1987) Biophys Chem 265:1275).

Examples of techniques for detecting differences of at least one nucleotide between 2 nucleic acids include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide probes may be prepared in which the known polymorphic nucleotide is placed centrally (allele-specific probes) and then hybridized to target DNA under conditions which permit hybridization only if a perfect match is found (Saiki et al. (1986) Nature 324:163); Saiki et al (1989) Proc. Natl Acad. Sci USA 86:6230; and Wallace et al. (1979) Nucl. Acids Res. 6:3543). Such allele specific oligonucleotide hybridization techniques may be used for the simultaneous detection of several nucleotide changes in different polymorphic regions of gene. For example, oligonucleotides having nucleotide sequences of specific allelic variants are attached to a hybridizing membrane and this membrane is then hybridized with labeled sample nucleic acid. Analysis of the hybridization signal will then reveal the identity of the nucleotides of the sample nucleic acid.

Alternatively, allele specific amplification technology which depends on selective PCR amplification may be used. Oligonucleotides used as primers for specific amplification may carry the allelic variant of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs et al (1989) Nucleic Acids Res. 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner (1993) Tibtech 11:238; Newton et al. (1989) Nucl. Acids Res. 17:2503). This technique is also termed "PROBE" for Probe Oligo Base Extension. In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection (Gasparini et al (1992) Mol. Cell Probes 6:1).

In another embodiment, identification of the allelic variant is carried out using an oligonucleotide ligation assay (OLA), as described, e.g., in U.S. Pat. No. 4,998,617 and in Landegren, U. et al., Science 241:1077-1080 (1988). The OLA protocol uses two oligonucleotides which are designed to be capable of hybridizing to abutting

sequences of a single strand of a target. One of the oligonucleotides is linked to a separation marker, e.g,. biotinylated, and the other is detectably labeled. If the precise complementary sequence is found in a target molecule, the oligonucleotides will hybridize such that their termini abut, and create a ligation substrate. Ligation then permits the labeled oligonucleotide to be recovered using avidin, or another biotin ligand. Nickerson, D. A. et al. have described a nucleic acid detection assay that combines attributes of PCR and OLA (Nickerson, D. A. et al., Proc. Natl. Acad. Sci. (U.S.A.) 87:8923-8927 (1990). In this method, PCR is used to achieve the exponential amplification of target DNA, which is then detected using OLA.

Several techniques based on this OLA method have been developed and can be used to detect specific allelic variants of a polymorphic region of a gene. For example, U.S. Pat. No. 5,593,826 discloses an OLA using an oligonucleotide having 3'-amino group and a 5'-phosphorylated oligonucleotide to form a conjugate having a phosphoramidate linkage. In another variation of OLA described in Tobe et al. ((1996)Nucleic Acids Res 24: 3728), OLA combined with PCR permits typing of two alleles in a single microtiter well. By marking each of the allele-specific primers with a unique hapten, i.e. digoxigenin and fluorescein, each LA reaction can be detected by using hapten specific antibodies that are labeled with different enzyme reporters, alkaline phosphatase or horseradish peroxidase. This system permits the detection of the two alleles using a high throughput format that leads to the production of two different colors.

The invention further provides methods for detecting single nucleotide polymorphisms in a gene. Because single nucleotide polymorphisms constitute sites of variation flanked by regions of invariant sequence, their analysis requires no more than the determination of the identity of the single nucleotide present at the site of variation and it is unnecessary to determine a complete gene sequence for each patient. Several methods have been developed to facilitate the analysis of such single nucleotide polymorphisms.

In one embodiment, the single base polymorphism can be detected by using a specialized exonuclease-resistant nucleotide, as disclosed, e.g., in Mundy, C. R. (U.S. Pat. No. 4,656,127). According to the method, a primer complementary to the allelic sequence immediately 3' to the polymorphic site is permitted to hybridize to a target molecule obtained from a particular animal or human. If the polymorphic site on the target molecule contains a nucleotide that is complementary to the particular exonuclease-resistant nucleotide derivative present, then that derivative will be incorporated onto the end of the hybridized primer. Such incorporation renders the primer resistant to exonuclease, and thereby permits its detection. Since the identity of the exonuclease-resistant derivative of the sample is known, a finding that the primer has become resistant to exonucleases reveals that the nucleotide present in the polymorphic site of the target molecule was complementary to that of the nucleotide derivative used in the reaction. This method has the advantage that it does not require the determination of large amounts of extraneous sequence data.

In another embodiment of the invention, a solution-based method is used for determining the identity of the nucleotide of a polymorphic site. Cohen, D. et al. (French Patent 2,650,840; PCT Appln. No. WO91/02087). As in the Mundy method of U.S. Pat. No. 4,656,127, a primer is employed that is complementary to allelic sequences immediately 3' to a polymorphic site. The method determines the identity of the nucleotide of that site using labeled dideoxynucleotide derivatives, which, if complementary to the nucleotide of the polymorphic site will become incorporated onto the terminus of the primer.

An alternative method, known as Genetic Bit Analysis or GBA TM is described by Goelet, P. et al. (PCT Appln. No. 92/15712). The method of Goelet, P. et al. uses mixtures of labeled terminators and a primer that is complementary to the sequence 3' to a polymorphic site. The labeled terminator that is incorporated is thus determined by, and complementary to, the nucleotide present in the polymorphic site of the target molecule being evaluated. In contrast to the method of Cohen et al. (French Patent 2,650,840; PCT Appln. No. WO91/02087) the method of Goelet, P. et

al. is preferably a heterogeneous phase assay, in which the primer or the target molecule is immobilized to a solid phase.

Recently, several primer-guided nucleotide incorporation procedures for assaying polymorphic sites in DNA have been described (Komher, J. S. et al., Nucl. Acids. Res. 17:7779-7784 (1989); Sokolov, B. P., Nucl. Acids Res. 18:3671 (1990); Syvanen, A. -C., et al., Genomics 8:684-692 (1990), Kuppuswamy, M. N. et al., Proc. Natl. Acad. Sci. (U.S.A.) 88:1143-1147 (1991); Prezant, T. R. et al., Hum. Mutat. 1:159-164 (1992); Ugozzoli, L. et al., GATA 9:107-112 (1992); Nyren, P. et al., Anal. Biochem. 208:171-175 (1993)). These methods differ from GBA TM in that they all rely on the incorporation of labeled deoxynucleotides to discriminate between bases at a polymorphic site. In such a format, since the signal is proportional to the number of deoxynucleotides incorporated, polymorphisms that occur in runs of the same nucleotide can result in signals that are proportional to the length of the run (Syvanen, A.-C., et al., Amer. J. Hum. Genet. 52:46-59 (1993)).

For determining the identity of the allelic variant of a polymorphic region located in the coding region of a gene, yet other methods than those described above can be used. For example, identification of an allelic variant which encodes a mutated gene protein can be performed by using an antibody specifically recognizing the mutant protein in, e.g., immunohistochemistry or immunoprecipitation. Antibodies to wild-type gene protein are described, e.g., in Acton et al. (1999) Science 271:518 (anti-mouse gene antibody cross-reactive with human gene). Other antibodies to wild-type gene or mutated forms of gene proteins can be prepared according to methods known in the art. Alternatively, one can also measure an activity of an gene protein, such as binding to a lipid or lipoprotein. Binding assays are known in the art and involve, e.g., obtaining cells from a subject, and performing binding experiments with a labeled lipid, to determine whether binding to the mutated form of the receptor differs from binding to the wild-type of the receptor.

If a polymorphic region is located in an exon, either in a coding or non-coding region of the gene, the identity of the allelic variant can be determined by determining the molecular structure of the mRNA, pre-mRNA, or cDNA. The molecular structure can be determined using any of the above described methods for determining the molecular structure of the genomic DNA, e.g., sequencing and SSCP.

The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits, such as those described above, comprising at least one probe or primer nucleic acid described herein, which may be conveniently used, e.g., to determine whether a subject has or is at risk of developing a disease associated with a specific gene allelic variant.

Sample nucleic acid for using in the above-described diagnostic and prognostic methods can be obtained from any cell type or tissue of a subject. For example, a subject's bodily fluid (e.g. blood) can be obtained by known techniques (e.g. venipuncture) or from human tissues like heart (biopsies, transplanted organs). Alternatively, nucleic acid tests can be performed on dry samples (e.g. hair or skin). Fetal nucleic acid samples for prenatal diagnostics can be obtained from maternal blood as described in International Patent Application No.WO91/07660 to Bianchi. Alternatively, amniocytes or chorionic villi may be obtained for performing prenatal testing.

Diagnostic procedures may also be performed in situ directly upon tissue sections (fixed and/or frozen) of patient tissue obtained from biopsies or resections, such that no nucleic acid purification is necessary. Nucleic acid reagents may be used as probes and/or primers for such in situ procedures (see, for example, Nuovo, G. J., 1992, PCR in situ hybridization: protocols and applications, Raven Press, New York).

In addition to methods which focus primarily on the detection of one nucleic acid sequence, profiles may also be assessed in such detection schemes. Fingerprint

profiles may be generated, for example, by utilizing a differential display procedure, Northern analysis and/or RT-PCR.

In practicing the present invention, the distribution of polymorphic patterns in a large number of individuals exhibiting particular markers of cardiovascular status or drug response is determined by any of the methods described above, and compared with the distribution of polymorphic patterns in patients that have been matched for age, ethnic origin, and/or any other statistically or medically relevant parameters, who exhibit quantitatively or qualitatively different status markers. Correlations are achieved using any method known in the art, including nominal logistic regression, chi square tests or standard least squares regression analysis. In this manner, it is possible to establish statistically significant correlations between particular polymorphic patterns and particular cardiovascular statuses (given in p values). It is further possible to establish statistically significant correlations between particular polymorphic patterns and changes in cardiovascular status or drug response such as, would result, e.g., from particular treatment regimens. In this manner, it is possible to correlate polymorphic patterns with responsivity to particular treatments.

In another embodiment of the present invention two or more polymorphic regions are combined to define so called 'haplotypes' . Haplotypes are groups of two or more SNPs that are functionally and/or spatially linked. It is possible to combine SNPs that are disclosed in the present invention either with each other or with additional polymorphic regions to form a haplotype. Haplotypes are expected to give better predictive/diagnostic information than a single SNP.

In a preferred embodiment of the present invention a panel of SNPs/haplotypes is defined that predicts the risk for CVD or drug response. This predictive panel is then used for genotyping of patients on a platform that can genotype multiple SNPs at the same time (Multiplexing). Preferred platforms are e.g. gene chips (Affymetrix) or the Luminex LabMAP reader. The subsequent identification and evaluation of a patient's haplotype can then help to guide specific and individualized therapy.

For example the present invention can identify patients exhibiting genetic polymorphisms or haplotypes which indicate an increased risk for adverse drug reactions. In that case the drug dose should be lowered in a way that the risk for ADR is diminished. Also if the patient's response to drug administration is particularly high (or the patient is badly metabolizing the drug), the drug dose should be lowered to avoid the risk of ADR.

In turn if the patient's response to drug administration is low (or the patient is a particularly high metabolizer of the drug), and there is no evident risk of ADR, the drug dose should be raised to an efficacious level.

It is self evident that the ability to predict a patient's individual drug response should affect the formulation of a drug, i.e. drug formulations should be tailored in a way that they suit the different patient classes (low/high responder, poor/good metabolizer, ADR prone patients). Those different drug formulations may encompass different doses of the drug, i.e. the medicinal products contains low or high amounts of the active substance. In another embodiement of the invention the drug formulation may contain additional substances that facilitate the beneficial effects and/or diminish the risk for ADR (Folkers et al. 1991, US Pat. 5,316,765).

Isolated Polymorphic Nucleic Acids, Probes, and Vectors

The present invention provides isolated nucleic acids comprising the polymorphic positions described herein for human genes; vectors comprising the nucleic acids; and transformed host cells comprising the vectors. The invention also provides probes which are useful for detecting these polymorphisms.

In practicing the present invention, many conventional techniques in molecular biology, microbiology, and recombinant DNA, are used. Such techniques are well known and are explained fully in, for example, Sambrook et al., 1989, Molecular

Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York; DNA Cloning: A Practical Approach, Volumes I and II, 1985 (D. N. Glover ed.); Oligonucleotide Synthesis, 1984, (M. L.Gait ed.); Nucleic Acid Hybridization, 1985, (Hames and Higgins); Ausubel et al., Current Protocols in Molecular Biology, 1997, (John Wiley and Sons); and Methods in Enzymology Vol. 154 and Vol. 155 (Wu and Grossman, and Wu, eds., respectively).

Insertion of nucleic acids (typically DNAs) comprising the sequences in a functional surrounding like full length cDNA of the present invention into a vector is easily accomplished when the termini of both the DNAs and the vector comprise compatible restriction sites. If this cannot be done, it may be necessary to modify the termini of the DNAs and/or vector by digesting back single-stranded DNA overhangs generated by restriction endonuclease cleavage to produce blunt ends, or to achieve the same result by filling in the single-stranded termini with an appropriate DNA polymerase.

Alternatively, any site desired may be produced, e.g., by ligating nucleotide sequences (linkers) onto the termini. Such linkers may comprise specific oligonucleotide sequences that define desired restriction sites. Restriction sites can also be generated by the use of the polymerase chain reaction (PCR). See, e.g., Saiki et al., 1988, Science 239:48. The cleaved vector and the DNA fragments may also be modified if required by homopolymeric tailing.

The nucleic acids may be isolated directly from cells or may be chemically synthesized using known methods. Alternatively, the polymerase chain reaction (PCR) method can be used to produce the nucleic acids of the invention, using either chemically synthesized strands or genomic material as templates. Primers used for PCR can be synthesized using the sequence information provided herein and can further be designed to introduce appropriate new restriction sites, if desirable, to facilitate incorporation into a given vector for recombinant expression.

The nucleic acids of the present invention may be flanked by native gene sequences, or may be associated with heterologous sequences, including promoters, enhancers, response elements, signal sequences, polyadenylation sequences, introns, 5'- and 3'-noncoding regions, and the like. The nucleic acids may also be modified by many means known in the art. Non-limiting examples of such modifications include methylation, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoroamidates, carbamates, morpholines etc.) and with charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.). Nucleic acids may contain one or more additional covalently linked moieties, such as, for example, proteins (e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), intercalators (e.g., acridine, psoralen, etc.), chelators (e.g., metals, radioactive metals, iron, oxidative metals, etc.), and alkylators. PNAs are also included. The nucleic acid may be derivatized by formation of a methyl or ethyl phosphotriester or an alkyl phosphoramidate linkage. Furthermore, the nucleic acid sequences of the present invention may also be modified with a label capable of providing a detectable signal, either directly or indirectly. Exemplary labels include radioisotopes, fluorescent molecules, biotin, and the like.

The invention also provides nucleic acid vectors comprising the gene sequences or derivatives or fragments thereof of genes described in the Examles. A large number of vectors, including plasmid and fungal vectors, have been described for replication and/or expression in a variety of eukaryotic and prokaryotic hosts, and may be used for gene therapy as well as for simple cloning or protein expression. Non-limiting examples of suitable vectors include without limitation pUC plasmids, pET plasmids (Novagen, Inc., Madison, Wis.), or pRSET or pREP (Invitrogen, San Diego, Calif.), and many appropriate host cells, using methods disclosed or cited herein or otherwise known to those skilled in the relevant art. The particular choice of vector/host is not critical to the practice of the invention.

Suitable host cells may be transformed/transfected/infected as appropriate by any suitable method including electroporation, $CaCl_2$ mediated DNA uptake, fungal or viral infection, microinjection, microprojectile, or other established methods. Appropriate host cells included bacteria, archebacteria, fungi, especially yeast, and plant and animal cells, especially mammalian cells. A large number of transcription initiation and termination regulatory regions have been isolated and shown to be effective in the transcription and translation of heterologous proteins in the various hosts. Examples of these regions, methods of isolation, manner of manipulation, etc. are known in the art. Under appropriate expression conditions, host cells can be used as a source of recombinantly produced peptides and polypeptides encoded by genes of the Examples. Nucleic acids encoding peptides or polypeptides from gene sequences of the Examples may also be introduced into cells by recombination events. For example, such a sequence can be introduced into a cell and thereby effect homologous recombination at the site of an endogenous gene or a sequence with substantial identity to the gene. Other recombination-based methods such as non-homologous recombinations or deletion of endogenous genes by homologous recombination may also be used.

In case of proteins that form heterodimers or other multimers, both or all subunits have to be expressed in one system or cell.

The nucleic acids of the present invention find use as probes for the detection of genetic polymorphisms and as templates for the recombinant production of normal or variant peptides or polypeptides encoded by genes listed in the Examples.

Probes in accordance with the present invention comprise without limitation isolated nucleic acids of about 10-100 bp, preferably 15-75 bp and most preferably 17-25 bp in length, which hybridize at high stringency to one or more of the polymorphic sequences disclosed herein or to a sequence immediately adjacent to a polymorphic position. Furthermore, in some embodiments a full-length gene sequence may be

used as a probe. In one series of embodiments, the probes span the polymorphic positions in genes disclosed herein. In another series of embodiments, the probes correspond to sequences immediately adjacent to the polymorphic positions.

<u>Polymorphic Polypeptides and Polymorphism-Specific Antibodies</u>

The present invention encompasses isolated peptides and polypeptides encoded by genes listed in the Examples comprising polymorphic positions disclosed herein. In one preferred embodiment, the peptides and polypeptides are useful screening targets to identify cardiovascular drugs. In another preferred embodiments, the peptides and polypeptides are capable of eliciting antibodies in a suitable host animal that react specifically with a polypeptide comprising the polymorphic position and distinguish it from other polypeptides having a different sequence at that position.

Polypeptides according to the invention are preferably at least five or more residues in length, preferably at least fifteen residues. Methods for obtaining these polypeptides are described below. Many conventional techniques in protein biochemistry and immunology are used. Such techniques are well known and are explained in Immunochemical Methods in Cell and Molecular Biology, 1987 (Mayer and Waler, eds; Academic Press, London); Scopes, 1987, Protein Purification: Principles and Practice, Second Edition (Springer-Verlag, N.Y.) and Handbook of Experimental Immunology, 1986, Volumes I-IV (Weir and Blackwell eds.).

Nucleic acids comprising protein-coding sequences can be used to direct the ITT recombinant expression of polypeptides encoded by genes disclosed herein in intact cells or in cell-free translation systems. The known genetic code, tailored if desired for more efficient expression in a given host organism, can be used to synthesize oligonucleotides encoding the desired amino acid sequences. The polypeptides may be isolated from human cells, or from heterologous organisms or cells (including, but not limited to, bacteria, fungi, insect, plant, and mammalian cells) into which an

appropriate protein-coding sequence has been introduced and expressed. Furthermore, the polypeptides may be part of recombinant fusion proteins.

Peptides and polypeptides may be chemically synthesized by commercially available automated procedures, including, without limitation, exclusive solid phase synthesis, partial solid phase methods, fragment condensation or classical solution synthesis. The polypeptides are preferably prepared by solid phase peptide synthesis as described by Merrifield, 1963, J. Am. Chem. Soc. 85:2149.

Methods for polypeptide purification are well-known in the art, including, without limitation, preparative disc-gel electrophoresis, isoelectric focusing, HPLC, reversed-phase HPLC, gel filtration, ion exchange and partition chromatography, and countercurrent distribution. For some purposes, it is preferable to produce the polypeptide in a recombinant system in which the protein contains an additional sequence tag that facilitates purification, such as, but not limited to, a polyhistidine sequence. The polypeptide can then be purified from a crude lysate of the host cell by chromatography on an appropriate solid-phase matrix. Alternatively, antibodies produced against peptides encoded by genes disclosed herein, can be used as purification reagents. Other purification methods are possible.

The present invention also encompasses derivatives and homologues of the polypeptides. For some purposes, nucleic acid sequences encoding the peptides may be altered by substitutions, additions, or deletions that provide for functionally equivalent molecules, i.e., function-conservative variants. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of similar properties, such as, for example, positively charged amino acids (arginine, lysine, and histidine); negatively charged amino acids (aspartate and glutamate); polar neutral amino acids; and non-polar amino acids.

The isolated polypeptides may be modified by, for example, phosphorylation, sulfation, acylation, or other protein modifications. They may also be modified with

a label capable of providing a detectable signal, either directly or indirectly, including, but not limited to, radioisotopes and fluorescent compounds.

The present invention also encompasses antibodies that specifically recognize the polymorphic positions of the invention and distinguish a peptide or polypeptide containing a particular polymorphism from one that contains a different sequence at that position. Such polymorphic position-specific antibodies according to the present invention include polyclonal and monoclonal antibodies. The antibodies may be elicited in an animal host by immunization with peptides encoded by genes disclosed herein or may be formed by in vitro immunization of immune cells. The immunogenic components used to elicit the antibodies may be isolated from human cells or produced in recombinant systems. The antibodies may also be produced in recombinant systems programmed with appropriate antibody-encoding DNA. Alternatively, the antibodies may be constructed by biochemical reconstitution of purified heavy and light chains. The antibodies include hybrid antibodies (i.e., containing two sets of heavy chain/light chain combinations, each of which recognizes a different antigen), chimeric antibodies (i.e., in which either the heavy chains, light chains, or both, are fusion proteins), and univalent antibodies (i.e., comprised of a heavy chain/light chain complex bound to the constant region of a second heavy chain). Also included are Fab fragments, including Fab' and F(ab).sub.2 fragments of antibodies. Methods for the production of all of the above types of antibodies and derivatives are well-known in the art and are discussed in more detail below. For example, techniques for producing and processing polyclonal antisera are disclosed in Mayer and Walker, 1987, Immunochemical Methods in Cell and Molecular Biology, (Academic Press, London). The general methodology for making monoclonal antibodies by hybridomas is well known. Immortal antibody-producing cell lines can be created by cell fusion, and also by other techniques such as direct transformation of B lymphocytes with oncogenic DNA, or transfection with Epstein-Barr virus. See, e.g., Schreier et al., 1980, Hybridoma Techniques; U.S. Pat. Nos. 4,341,761; 4,399,121; 4,427,783; 4,444,887; 4,466,917; 4,472,500; 4,491,632; and 4,493,890. Panels of monoclonal antibodies produced against peptides encoded

by genes disclosed herein can be screened for various properties; i.e. for isotype, epitope affinity, etc.

The antibodies of this invention can be purified by standard methods, including but not limited to preparative disc-gel electrophoresis, isoelectric focusing, HPLC, reversed-phase HPLC, gel filtration, ion exchange and partition chromatography, and countercurrent distribution. Purification methods for antibodies are disclosed, e.g., in The Art of Antibody Purification, 1989, Amicon Division, W. R. Grace & Co. General protein purification methods are described in Protein Purification: Principles and Practice, R. K. Scopes, Ed., 1987, Springer-Verlag, New York, N.Y.

Methods for determining the immunogenic capability of the disclosed sequences and the characteristics of the resulting sequence-specific antibodies and immune cells are well-known in the art. For example, antibodies elicited in response to a peptide comprising a particular polymorphic sequence can be tested for their ability to specifically recognize that polymorphic sequence, i.e., to bind differentially to a peptide or polypeptide comprising the polymorphic sequence and thus distinguish it from a similar peptide or polypeptide containing a different sequence at the same position.

Kits

As set forth herein, the invention provides diagnostic methods, e.g., for determining the identity of the allelic variants of polymorphic regions present in the gene loci of genes disclosed herein, wherein specific allelic variants of the polymorphic region are associated with cardiovascular diseases. In a preferred embodiment, the diagnostic kit can be used to determine whether a subject is at risk of developing a cardiovascular disease. This information could then be used, e.g., to optimize treatment of such individuals.

In preferred embodiments, the kit comprises a probe or primer which is capable of hybridizing to a gene and thereby identifying whether the gene contains an allelic variant of a polymorphic region which is associated with a risk for cardiovascular disease. The kit preferably further comprises instructions for use in diagnosing a subject as having, or having a predisposition, towards developing a cardiovascular disease. The probe or primers of the kit can be any of the probes or primers described in this file.

Preferred kits for amplifying a region of a gene comprising a polymorphic region of interest comprise one, two or more primers.

Antibody-based diagnostic methods and kits:

The invention also provides antibody-based methods for detecting polymorphic patterns in a biological sample. The methods comprise the steps of: (i) contacting a sample with one or more antibody preparations, wherein each of the antibody preparations is specific for a particular polymorphic form of the proteins encoded by genes disclosed herein, under conditions in which a stable antigen-antibody complex can form between the antibody and antigenic components in the sample; and (ii) detecting any antigen-antibody complex formed in step (i) using any suitable means known in the art, wherein the detection of a complex indicates the presence of the particular polymorphic form in the sample.

Typically, immunoassays use either a labelled antibody or a labelled antigenic component (e.g., that competes with the antigen in the sample for binding to the antibody). Suitable labels include without limitation enzyme-based, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays that amplify the signals from the probe are also known, such as, for example, those that utilize biotin and avidin, and enzyme-labelled immunoassays, such as ELISA assays.

The present invention also provides kits suitable for antibody-based diagnostic applications. Diagnostic kits typically include one or more of the following components:

(i) Polymorphism-specific antibodies. The antibodies may be pre-labelled; alternatively, the antibody may be unlabelled and the ingredients for labelling may be included in the kit in separate containers, or a secondary, labelled antibody is provided; and

(ii) Reaction components: The kit may also contain other suitably packaged reagents and materials needed for the particular immunoassay protocol, including solid-phase matrices, if applicable, and standards.

The kits referred to above may include instructions for conducting the test. Furthermore, in preferred embodiments, the diagnostic kits are adaptable to high-throughput and/or automated operation.

Drug Targets and Screening Methods

According to the present invention, nucleotide sequences derived from genes disclosed herein and peptide sequences encoded by genes disclosed herein, particularly those that contain one or more polymorphic sequences, comprise useful targets to identify cardiovascular drugs, i.e., compounds that are effective in treating one or more clinical symptoms of cardiovascular disease. Furthermore, especially when a protein is a multimeric protein that are build of two or more subunits, is a combination of different polymorphic subunits very useful.

Drug targets include without limitation (i) isolated nucleic acids derived from the genes disclosed herein, and (ii) isolated peptides and polypeptides encoded by genes disclosed herein, each of which comprises one or more polymorphic positions.

In vitro screening methods:

In one series of embodiments, an isolated nucleic acid comprising one or more polymorphic positions is tested in vitro for its ability to bind test compounds in a sequence-specific manner. The methods comprise:

(i) providing a first nucleic acid containing a particular sequence at a polymorphic position and a second nucleic acid whose sequence is identical to that of the first nucleic acid except for a different sequence at the same polymorphic position;

(ii) contacting the nucleic acids with a multiplicity of test compounds under conditions appropriate for binding; and

(iii) identifying those compounds that bind selectively to either the first or second nucleic acid sequence.

Selective binding as used herein refers to any measurable difference in any parameter of binding, such as, e.g., binding affinity, binding capacity, etc.

In another series of embodiments, an isolated peptide or polypeptide comprising one or more polymorphic positions is tested in vitro for its ability to bind test compounds in a sequence-specific manner. The screening methods involve:

(i) providing a first peptide or polypeptide containing a particular sequence at a polymorphic position and a second peptide or polypeptide whose sequence is identical to the first peptide or polypeptide except for a different sequence at the same polymorphic position;

(ii) contacting the polypeptides with a multiplicity of test compounds under conditions appropriate for binding; and

(iii) identifying those compounds that bind selectively to one of the nucleic acid sequences.

In preferred embodiments, high-throughput screening protocols are used to survey a large number of test compounds for their ability to bind the genes or peptides disclosed above in a sequence-specific manner.

Test compounds are screened from large libraries of synthetic or natural compounds. Numerous means are currently used for random and directed synthesis of saccharide, peptide, and nucleic acid based compounds. Synthetic compound libraries are commercially available from Maybridge Chemical Co. (Trevillet, Cornwall, UK), Comgenex (Princeton, N.J.), Brandon Associates (Merrimack, N.H.), and Microsource (New Milford, Conn.). A rare chemical library is available from Aldrich (Milwaukee, Wis.). Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available from e.g. Pan Laboratories (Bothell, Wash.) or MycoSearch (N.C.), or are readily producible. Additionally, natural and synthetically produced libraries and compounds are readily modified through conventional chemical, physical, and biochemical means.

In vivo screening methods

Intact cells or whole animals expressing polymorphic variants of genes disclosed herein can be used in screening methods to identify candidate cardiovascular drugs.

In one series of embodiments, a permanent cell line is established from an individual exhibiting a particular polymorphic pattern. Alternatively, cells (including without limitation mammalian, insect, yeast, or bacterial cells) are programmed to express a gene comprising one or more polymorphic sequences by introduction of appropriate DNA. Identification of candidate compounds can be achieved using any suitable assay, including without limitation (i) assays that measure selective binding of test

compounds to particular polymorphic variants of proteins encoded by genes disclosed herein; (ii) assays that measure the ability of a test compound to modify (i.e., inhibit or enhance) a measurable activity or function of proteins encoded by genes disclosed herein; and (iii) assays that measure the ability of a compound to modify (i.e., inhibit or enhance) the transcriptional activity of sequences derived from the promoter (i.e., regulatory) regions of genes disclosed herein.

In another series of embodiments, transgenic animals are created in which (i) one or more human genes disclosed herein, having different sequences at particular polymorphic positions are stably inserted into the genome of the transgenic animal; and/or (ii) the endogenous genes disclosed herein are inactivated and replaced with human genes disclosed herein, having different sequences at particular polymorphic positions. See, e.g., Coffman, Semin. Nephrol. 17:404, 1997; Esther et al., Lab. Invest. 74:953, 1996; Murakami et al., Blood Press. Suppl. 2:36, 1996. Such animals can be treated with candidate compounds and monitored for one or more clinical markers of cardiovascular status.

The following are intended as non-limiting examples of the invention.

Material and Methods

Genotyping of patient DNA with the Pyrosequencing™ Method as described in the patent application WO 9813523:

First a PCR is set up to amplify the flanking regions around a SNP. Therefor 2 ng of genomic DNA (patient sample) are mixed with a primerset (20 – 40 pmol) producing a 75 to 320 bp PCR fragment with 0,3 to 1 U Qiagens Hot Star Taq Polymerase™ in a total volume of 20 µL. One primer is biotinylated depending on the direction of the sequencing primer. To force the biotinylated primer to be incorporated it is used 0,8 fold.

For primer design, programms like Oligo 6™ (Molecular Biology Insights) or Primer Select™ (DNAStar) are used. PCR setup is performed by a BioRobot 3000 ™ from Qiagen. PCR takes place in T1 or Tgradient Thermocyclers ™ from Biometra.

The whole PCR reaction is transferred into a PSQ plate ™ (Pyrosequencing) and prepared using the Sample Prep Tool ™ and SNP Reagent Kit ™ from Pyrosequencing according to their instructions.

<u>Preparation of template for Pyrosequencing™:</u>

Sample preparation using PSQ 96 Sample Prep Tool:

1. Mount the PSQ 96 Sample Prep Tool Cover onto the PSQ 96 Sample Prep Tool as follows: Place the cover on the desk, retract the 4 attachment rods by separating the handle from the magnetic rod holder, fit the magnetic rods into the holes of the cover plate, push the handle downward until a click is heard. The PSQ 96 Sample Prep Tool is now ready for use.

2. To transfer beads from one plate to another, place the covered tool into the PSQ 96 Plate containing the samples and lower the magnetic rods by separating the handle from the magnetic rod holder. Move the tool up and down a few times then wait for 30-60 seconds. Transfer the beads into a new PSQ 96 plate containing the solution of choice.

3. Release the beads by lifting the magnetic rod holder, bringing it together with the handle. Move the tool up and down a few times to make sure that the beads are released.

All steps are performed at room temperature unless otherwise stated.

Immobilization of PCR product:

Biotinylated PCR products are immobilized on streptavidin-coated Dynabeads™ M-280 Streptavidin. Parallel immobilization of several samples are performed in the PSQ 96 Plate.

1. Mix PCR product, 20 µl of a well optimized PCR, with 25 µl 2X BW-buffer II. Add 60-150 µg Dynabeads. It is also possible to add a mix of Dynabeads and 2X BW-buffer II to the PCR product yielding a final BW-buffer II concentration of approximately 1x.

2. Incubate at 65°C for 15 min agitation constantly to keep the beads dispersed. For optimal immobilization of fragments longer than 300 bp use 30 min incubation time.

Strand separation:

4. For strand separation, use the PSQ 96 Sample Prep Tool to transfer the beads with the immobilized sample to a PSQ 96 Plate containing 50 µl 0.50 M NaOH per well. Release the beads.
5. After approximately 1 min, transfer the beads with the immobilized strand to a PSQ 96 Plate containing 99 µl 1x Annealing buffer per well and mix thoroughly.
6. Transfer the beads to a PSQ 96 Plate containing 45 µl of a mix of 1x Annealing buffer and 3-15 pmoles sequencing primer per well.
7. Heat at 80°C for 2 minutes in the PSQ 96 Sample Prep Thermoplate and move to room temperature.
8. After reaching room temperature, continue with the sequencing reaction.

Sequencing reaction:

1. Choose the method to be used ("SNP Method") and enter relevant information in the PSQ 96 Instrument Control software.
2. Place the cartridge and PSQ 96 Plate in the PSQ 96 Instrument.
3. Start the run.

Genotyping using the ABI 7700/7900 instrument (TaqMan)

SNP genotypisation using the TaqMan (Applied Biosystems/Perkin Elmer) was performed according to the manufacturer's instructions. The TaqMan assay is discussed by Lee et al., Nucleic Acids Research 1993, 21: 3761-3766.

Genotyping with a service contractor:

Qiagen Genomics, formerly Rapigene, is a service contractor for genotyping SNPs in patient samples. Their method is based on a primer extension method where two complementary primers are designed for each genotype that are labeled with different tags. Depending on the genotype only one primer will be elongated together with a certain tag. This tag can be detected with mass spectrometry and is a measure for the respective genotype. The method is described in the following patent: "Detection and identification of nucleic acid molecules - using tags which may be detected by non-fluorescent spectrometry or potentiometry" (WO 9727325).

Examples

To exemplify the present invention and it's utility (the imaginary) baySNP 28 will be used in the following:

The nucleotide polymorphism found for baySNP 28 (e.g. C to T exchange) and the gene in which it presumably resides can be read from table 3. baySNP 28 was genotyped in various patient cohorts using primers as described in table 2. As a result the following number of patients carrying different genotypes were found (information combined from tables 3 and 5a):

baySNP	Cohort	Total	Genotype 11 "CC"	Genotype 12 "CT"	Genotype 22 "TT"
28	HELD_FEM_HIRESP	12	1	2	9
28	HELD_FEM_LORESP	22	3	12	7

When comparing the number of female patients exhibiting a high response to statin therapy (HELD_FEM_HIRESP) with the control cohort (HELD_FEM_LORESP) it appears that the number of low responders carrying the CT genotype is increased. This points to a lower statin response among female individuals with the CT genotype. Applying statistical tests on those findings the following p-values were obtained (data taken from table 5b):

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL
28	HELD_FEM_EFF	0,0506	0,0508	0,0442

As at least one of the GTYPE p values is below 0,05 the association of genotype and statin response phenotype is regarded as statistically significant. I.e. the analysis of a patient's genotype can predict the response to statin therapy. In more detail one can

calculate the relative risk to exhibit a certain statin response phenotype when carrying a certain genotype (data taken from table 6a):

BAYSNP	COMPARISON	GTYPE1	GTYPE2	GTYPE3	RR1	RR2	RR3
28	HELD_FEM_EFF	CC	CT	TT	0,68	0,29	3,38

In case of baySNP 28 the risk to exhibit a high responder phenotype is 3,38 times higher when carrying the TT genotype. This indicates that a TT polymorphism in baySNP 28 is an independent risk factor for high statin response in females. On the other hand carriers of a CT or CC genotype have a reduced risk of being a high responder.

In addition statistical associations can be calculated on the basis on alleles. This calculation would identify risk alleles instead of risk genotypes.
In case of baySNP 28 the following allele counts were obtained (data combined from tables 3 and 5a):

baySNP	Cohort	Total	Allele 1 "C"	Allele 2 "T"
28	HELD_FEM_HIRESP	12	4	20
28	HELD_FEM_LORESP	22	18	26

When comparing the number of female patients with high statin response (HELD_FEM_HIRESP) with the control cohort (HELD_FEM_LORESP) it appears that the number of high responders carrying the T allele is increased, whereas the number of high responders carrying the C allele is diminished. This points to a higher statin response among female individuals with the T allele. Applying statistical tests on those findings the following p-values were obtained (data taken from table 5b):

BAYSNP	COMPARISON	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
28	HELD_FEM_EFF	0,0411	0,0579	0,0349

As at least one of the ALLELE p values is below 0,05 the association of allele and statin response phenotype is regarded as statistically significant (in this example significant p values were obtained from two statistical tests). I.e. also the analysis of a patient's alleles from baySNP 28 can predict the extend of statin response. In more detail one can calculate the relative risk to exhibit a certain statin response phenotype when carrying a certain allele (data taken from table 6b):

baySNP	Allele 1	Allele 2	COMPARISON	RR1	RR2
28	C	T	HELD_FEM_EFF	0,42	2,39

In case of baySNP 28 the risk to exhibit a high responder phenotype is 2,39 times higher when carrying the T allele. This indicates that the T allele of baySNP28 is an independent risk factor for a high statin response in females. In other words those patients should receive lower doses of statins in order to avoid ADR. However due to their 'high responder' phenotype they will still benefit from the drug. In turn carriers of the C allele should receive higher drug doses in order to experience a benefical therapeutic effect.

Another example is (the imaginary) baySNP 29, which is taken to exemplify polymorphisms relevant for adverse drug reactions. baySNP 29 was found significant when comparing male patients with severe ADR to the respective controls (as defined in table 1b).

The relative risk ratios for the genotypes AA, AG and GG were as follows (data taken from table 6a):

BAYSNP	COMPARISON	GTYPE1	GTYPE2	GTYPE3	RR1	RR2	RR3
29	HELD_MAL_ADR5ULN	AA	AG	GG	3,15	0,66	0,32

In this case male patients carrying the AA genotype have a 3,15 times higher risk to suffer from ADR. In other words those patients should either receive lower doses of statins or switch to an alternative therapy in order to avoid ADR. On the other hand male patients with AG or GG genotypes appear to be more resistant to ADR and hence better tolerate statin therapy.

As can be seen from the following tables some of the associations that are disclosed in the present invention are indicative for more than one phenotype. Some baySNPs can for example be linked to ADR, but also to the risk to suffer from CVD (table 6).

Sequences

The sequence section contains all phenotype associated ('PA') SNPs and adjacent genomic sequences. The position of the polymorphisms that were used for the association studies ('baySNP') is indicated. Sometimes additional variations are found in the surrounding genomic sequence, that are marked by it's respective IUPAC code. Although those surrounding SNPs were not explicitly analyzed, they likely exihibit a similar association to a phenotype as the baySNP (due to linkage disequillibrium, Reich D.E. et al. Nature 411, 199-204, 2001).

Table 1a Definition of "good" and "bad" serum lipid levels

	"Good"	"Bad"
LDL-Cholesterol [mg/dL]	125 -150	170 - 200
Cholesterol [mg/dL]	190 - 240	265 - 315
HDL-Cholesterol [mg/dL]	60 -105	30 - 55
Triglycerides [mg/dL]	45 - 115	170 – 450

Table 1b Definition of drug response phenotypes

Low responder	Decrease of serum LDL of at least 10% and at most 50% upon administration of 0.8 mg Cerivastatin (female patients)
High responder	Decrease of serum LDL of at least 50% upon administration of 0.4 mg Cerivastatin (female patients)
Very low responder	Decrease of serum LDL of at least 10% and at most 35% upon administration of 0.8 mg Cerivastatin (female patients)
Very high responder	Decrease of serum LDL of at least 55% upon administration of 0.4 mg Cerivastatin (female patients)
Ultra low responder	Decrease of serum LDL of at least 10% and at most 25% upon administration of 0.8 mg Cerivastatin (female patients)
Ultra high responder	Decrease of serum LDL of at least 60% upon administration of 0.4 mg Cerivastatin (female patients)
Tolerant patient	No diagnosis of muscle cramps, muscle pain, muscle weakness, myalgia or myopathy AND serum CK levels below 70 mg/dl in women and below 80 mg/dl in men.
ADR patient (CK increase at least 2×ULN)	Diagnosis of muscle cramps, muscle pain, muscle weakness, myalgia or myopathy OR serum CK levels higher than 140 mg/dl in women and 160 mg/dl in men.
Advanced ADR patient [ADR3] (advanced CK increase, at least 3×ULN)*	Serum CK levels higher than 210 mg/dl in women and 240 mg/dl in men
Severe ADR patient [ADR5] (severe CK increase, at least 5×ULN)*	Serum CK levels higher than 350 mg/dl in women and 400 mg/dl in men

*: When assembling the cohorts for advanced and severe ADR we focused on the CK serum levels as those provide a more independent measure of statin related ADR.

Table 1c Definition of "high" and "low" serum HDL cholesterol levels

	Male individuals	Female individuals
‚High' HDL-Cholesterol [mg/dL]	>=80	>=104
‚Low' HDL-Cholesterol [mg/dL]	<=35	<=37

An informed consent was signed by the patients and control people. Blood was taken by a physician according to medical standard procedures.
Samples were collected anonymous and labeled with a patient number.
DNA was extracted using kits from Qiagen.

Table 2 **Oligonucleotide primers used for genotyping**

Depending on the method used for genotyping different oligonucleotides were utilized. The table lists the various methods and primer sets that were used for this invention. Primers were designed using suitable programs like Primer Express™ (Applied Biosystems, Darmstadt, Germany) or Oligo™ (Molecular Biology Insights, Inc., Cascade, CO, USA).

Method	No. of oligonucleotides	Type of oligonucletides
Mass Spectrometry	4	2 Primers for preamplification of the genomic fragment, 2 allele specific primers with additional tag sequences for subsequent allele spec. PCR
Pyrosequencing™	3	2 Primers for preamplification of the genomic fragment (one biotinylated), 1 sequencing primer
TaqMan	4	2 Primers for amplification of the genomic fragment, 2 allele specific probes carrying different fluorochromes (VIC, FAM) and a quencher. Preferably the allele specific probes have a minor groove binder (MGB) attached (Kutyavin et al., Nucleic Acids Research 2000, 28:655-661).

Table 3 **PA SNPs, SNP classes and putative PA genes**

The baySNP number refers to an internal numbering of the PA SNPs. Listed are the different polymorphisms found in our association study. Also from the association study we defined SNP classes; with ADR being adverse drug reaction related, with EFF being drug efficacy related and CVD being cardiovascular disease related. ADR3 and ADR5 relate to advanced and severe ADR, whereas VEFF and UEFF relate to very high/low and ultra high/low drug efficacy (see table 1b). Also accession numbers and descriptions of those gene loci are given that are most homologous to the PA genes as listed in the sequences section (see below). Homologous genes and their accession numbers could be found by those skilled in the art in the Genbank database. The term 'SECONDARY' marks SNPs that do not reside inside the respective gene, but in it's proximity. Null: not defined.

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
29	CVD	AA	AG	GG	HS162961	Human T-lymphoma invasion and metastasis inducing TIAM1 protein (TIAM1) mRNA
29	ADR3	AA	AG	GG	HS162961	Human T-lymphoma invasion and metastasis inducing TIAM1 protein (TIAM1) mRNA
52	CVD	CC	CG	GG	X69907	H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form)
57	CVD	CC	CT	TT	M34175	Human beta adaptin mRNA, complete cds.
118	CVD	CC	CT	TT	X64229	H.sapiens dek mRNA
137	ADR5	GG	AG	AA	M64082	Human flavin-containing monooxygenase (FMO1) mRNA, complete cds.
137	ADR3	GG	AG	AA	M64082	Human flavin-containing monooxygenase (FMO1) mRNA, complete cds.
179	ADR5	GG	AG	AA	NM_000191	Homo sapiens 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethyl-glutaricaciduria) (HMGCL), mRNA
179	ADR3	GG	AG	AA	NM_000191	Homo sapiens 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethyl-glutaricaciduria) (HMGCL), mRNA
179	ADR	GG	AG	AA	NM_000191	Homo sapiens 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethyl-glutaricaciduria) (HMGCL), mRNA

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
240	ADR3	GG	CG	CC	X51757	Human heat-shock protein HSP70B` gene
241	ADR3	GG	AG	AA	X51757	Human heat-shock protein HSP70B` gene
241	ADR5	GG	AG	AA	X51757	Human heat-shock protein HSP70B` gene
288	CVD	GG	CG	CC	X79204	H.sapiens SCA1 mRNA for ataxin
384	CVD	CC	CG	GG	U12595	Human tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA, partial cds.
533	CVD	GG	AG	AA	X82895	H.sapiens mRNA for DLG2
542	ADR	GG	AG	AA	M64082	Human flavin-containing monooxygenase (FMO1) mRNA, complete cds.
576	CVD	CC	CT	null	D10667	Homo sapiens mRNA for smooth muscle myosin heavy chain, partial cds.
608	CVD	GG	AG	AA	M94363	Human lamin B2 (LAMB2) gene and ppv1 gene sequence.
614	CVD	GG	AG	AA	J04031	Human methylenetetrahydrofolate dehydrogenase- methenyltetrahydrofolate cyclohydrolase-formyltetrahydrofolate synthetase mRNA, complete cds.
738	CVD	AA	AC	CC	L43509	Homo sapiens methionine adenosyltransferase alpha subunit gene fragment.
1056	CVD	AA	AG	GG	Q16720	CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, ISOFORMS 3A/3B (EC 3.6.1.38) (CALCIUM PUMP) (PMCA3).
1092	ADR5	GG	CG	CC	M63971	Human vascular endothelial growth factor gene, exon 1.
1524	CVD	CC	AC	AA	AF223404	Homo sapiens WNT1 inducible signaling pathway protein 1 (WISP1) gene, promoter and partial cds.
1574	CVD	TT	CT	CC	M57965	Homo sapiens (clones lambda gMHC 1,2,3 and 4) beta-myosin heavy chain (MYH7) gene, complete cds.
1582	ADR3	TT	CT	CC	AF050163	Homo sapiens lipoprotein lipase precursor, gene, partial cds.
1657	EFF	CC	CT	TT	J02846	Human tissue factor gene, complete cds.
1722	CVD	TT	CT	CC	D73409	Homo sapiens mRNA for diacylglycerol kinase delta, complete cds.
1756	ADR5	CC	CT	TT	M64880	Human protein C inhibitor gene, complete cds.

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
175[illegible]	CVD	GG	AG	AA	J04046	Human calmodulin mRNA, complete cds.
175[illegible]	VEFF	GG	AG	AA	J04046	Human calmodulin mRNA, complete cds.
1757	ADR	GG	AG	AA	J04046	Human calmodulin mRNA, complete cds.
1765	CVD	AA	AG	GG	J05096	Human Na,K-ATPase subunit alpha 2 (ATP1A2) gene, complete cds.
1767	ADR3	TT	CT	CC	J05096	Human Na,K-ATPase subunit alpha 2 (ATP1A2) gene, complete cds.
1767	ADR5	TT	CT	CC	J05096	Human Na,K-ATPase subunit alpha 2 (ATP1A2) gene, complete cds.
1837	ADR3	CC	CT	TT	J00098	Human apolipoprotein A-I and C-III genes, complete cds.
1837	CVD	CC	CT	TT	J00098	Human apolipoprotein A-I and C-III genes, complete cds.
1837	ADR	CC	CT	TT	J00098	Human apolipoprotein A-I and C-III genes, complete cds.
1854	CVD	AA	AG	GG	M17712	Human cardiac myosin heavy chain mRNA, 3' end.
1862	CVD	CC	CT	TT	M92357	Homo sapiens B94 protein mRNA, complete cds.
2085	CVD	GG	GT	TT	X82540	H.sapiens mRNA for activin beta-C chain
2093	CVD	CC	CT	TT	X83543	H.sapiens APXL mRNA
2109	CVD	AA	AG	GG	Y09912	H.sapiens AP-2 beta gene
2124	CVD	GG	null	TT	Z30643	H.sapiens mRNA for chloride channel (putative) 2139bp
2140	UEFF	GG	GT	TT	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
2140	EFF	GG	GT	TT	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
2140	ADR	GG	GT	TT	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
2140	VEFF	GG	GT	TT	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
2141	ADR3	GG	AG	AA	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
2141	UEFF	GG	AG	AA	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
2141	ADR	GG	AG	AA	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
2186	ADR5	TT	CT	CC	M64880	Human protein C inhibitor gene, complete cds.

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
2187	ADR3	CC	CT	TT	M64880	Human protein C inhibitor gene, complete cds.
2192	ADR	GG	AG	AA	M21616	Human platelet-derived growth factor (PDGF) receptor mRNA, complete cds.
2192	ADR3	GG	AG	AA	M21616	Human platelet-derived growth factor (PDGF) receptor mRNA, complete cds.
2192	ADR5	GG	AG	AA	M21616	Human platelet-derived growth factor (PDGF) receptor mRNA, complete cds.
2203	CVD	TT	CT	CC	L36033	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds.
2217	CVD	GG	GT	TT	M15395	Human leukocyte adhesion protein (LFA-1/Mac-1/p150,95 family) beta subunit mRNA.
2281	CVD	AA	AC	CC	X87872	H.sapiens mRNA for hepatocyte nuclear factor 4c
2284	CVD	GG	AG	AA	AB021744	Homo sapiens XIIIA gene for coagulation factor XIII A subunit, promoter sequence.
2290	CVD	AA	AG	GG	M11309	Human coagulation factor IX mRNA, complete cds.
2327	ADR	AA	AC	CC	M63971	Human vascular endothelial growth factor gene, exon 1.
2327	ADR5	AA	AC	CC	M63971	Human vascular endothelial growth factor gene, exon 1.
2327	ADR3	AA	AC	CC	M63971	Human vascular endothelial growth factor gene, exon 1.
2327	EFF	AA	AC	CC	M63971	Human vascular endothelial growth factor gene, exon 1.
2353	CVD	AA	AG	GG	AJ246000	Homo sapiens mRNA for leucocyte adhesion receptor, L-selectin
2371	CVD	AA	AC	CC	Q92679	BETA-MYOSIN HEAVY CHAIN.
2376	CVD	CC	CT	null	M15856	Human lipoprotein lipase mRNA, complete cds.
2401	UEFF	TT	GT	GG	M18082	Human plasminogen activator inhibitor 2 (PAI-2) mRNA, complete cds.
2463	CVD	TT	CT	CC	AF084225	Homo sapiens cytochrome P450 2E1 (CYP2E1) mRNA, partial cds.
2755	ADR	AA	AG	GG	D63807	Human mRNA for lanosterol synthase, complete cds.
2755	EFF	AA	AG	GG	D63807	Human mRNA for lanosterol synthase, complete cds.
2925	VEFF	GG	AG	AA	J04501	Human muscle glycogen synthase mRNA, complete cds.
2925	UEFF	GG	AG	AA	J04501	Human muscle glycogen synthase mRNA, complete cds.
3043	ADR3	GG	AG	AA	U49248	ABCC2: ATP-binding cassette, sub-family C (CFTR/MRP), member 2

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
3152	VEFF	TT	AT	AA	L31573	Human sulfite oxidase mRNA, complete cds.
3214	VEFF	CC	CG	GG	L39211	Homo sapiens mitochondrial carnitine palmitoyltransferase I mRNA, complete cds.
3215	ADR5	CC	CG	null	L40027	Homo sapiens glycogen synthase kinase 3 mRNA, complete cds.
3237	CVD	CC	CG	GG	L41162	Homo sapiens collagen alpha 3 type IX (COL9A3) mRNA, complete cds.
3241	ADR	TT	CT	CC	L41668	Homo sapiens UDP-galactose-4-epimerase (GALE) mRNA, complete cds.
3826	ADR5	CC	AC	AA	BC006394	Homo sapiens, COX10 (yeast) homolog, cytochrome c oxidase assembly protein (heme A: farnesyltransferase)
3826	ADR3	CC	AC	AA	BC006394	Homo sapiens, COX10 (yeast) homolog, cytochrome c oxidase assembly protein (heme A: farnesyltransferase)
3842	CVD	CC	CG	null	U12595	Human tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA, partial cds.
3843	CVD	AA	AT	TT	U12595	Human tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA, partial cds.
3869	UEFF	GG	GT	TT	U17195	Homo sapiens A-kinase anchor protein (AKAP100) mRNA, complete cds.
3942	UEFF	CC	AC	AA	BC012063	Homo sapiens, Similar to retinoid X receptor, gamma, clone MGC:19909 IMAGE:4635470, mRNA, complete cds.
4018	CVD	TT	CT	CC	BC000011	Homo sapiens, mevalonate (diphospho) decarboxylase, clone MGC:1701 IMAGE:3505156, mRNA, complete cds.
4206	ADR3	AA	AT	TT	BC000006	Homo sapiens, ATPase, Na+/K+ transporting, beta 1 polypeptide
4206	ADR	AA	AT	TT	BC000006	Homo sapiens, ATPase, Na+/K+ transporting, beta 1 polypeptide
4206	ADR5	AA	AT	TT	BC000006	Homo sapiens, ATPase, Na+/K+ transporting, beta 1 polypeptide
4527	CVD	GG	AG	AA	X76228	H.sapiens mRNA for vacuolar H+ ATPase E subunit
4527	ADR3	GG	AG	AA	X76228	H.sapiens mRNA for vacuolar H+ ATPase E subunit
4527	ADR5	GG	AG	AA	X76228	H.sapiens mRNA for vacuolar H+ ATPase E subunit
4544	ADR3	GG	AG	AA	NM_000755	Homo sapiens carnitine acetyltransferase (CRAT), nuclear gene encoding mitochondrial

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
						protein, transcript variant 1, mRNA
4544	ADR	GG	AG	AA	NM_000755	Homo sapiens carnitine acetyltransferase (CRAT), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA
4545	ADR3	GG	AG	AA	NM_000755	Homo sapiens carnitine acetyltransferase (CRAT), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA
4545	ADR	GG	AG	AA	NM_000755	Homo sapiens carnitine acetyltransferase (CRAT), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA
4668	ADR5	CC	AC	AA	HSKINAANP	H.sapiens mRNA for kinase A anchor protein
4669	EFF	CC	CT	TT	HSKINAANP	H.sapiens mRNA for kinase A anchor protein
4718	CVD	GG	AG	AA	Y09862	H.sapiens mRNA for legumain
4818	CVD	GG	AG	AA	AJ276181	Homo sapiens partial ZNF202 gene for zinc finger protein homolog, exon 5
4827	ADR5	AA	AG	GG	L07033	Human hydroxymethylglutaryl-CoA lyase mRNA, complete cds.
4838	CVD	AA	AG	GG	L08246	Human myeloid cell differentiation protein (MCL1) mRNA.
4856	CVD	GG	AG	null	L11669	Human tetracycline transporter-like protein mRNA, complete cds.
4868	ADR	TT	CT	CC	U83661	Homo sapiens multidrug resistance protein 5 (MRP5) mRNA, complete cds
4868	ADR5	TT	CT	CC	U83661	Homo sapiens multidrug resistance protein 5 (MRP5) mRNA, complete cds
4887	CVD	CC	AC	AA	AC004264	Homo sapiens PAC clone RP1-102K2 from 22q12.1-qter, complete sequence.
4912	CVD	GG	AG	AA	M63971	Human vascular endothelial growth factor gene, exon 1.
4951	ADR3	GG	AG	AA	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
4951	ADR5	GG	AG	AA	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
4951	ADR	GG	AG	AA	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
4952	ADR3	TT	CT	CC	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
4952	ADR5	TT	CT	CC	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
4966	CVD	GG	AG	AA	AF133298	Homo sapiens cytochrome P450 (CYP4F8) mRNA, complete cds.
4966	ADR	GG	AG	AA	AF133298	Homo sapiens cytochrome P450 (CYP4F8) mRNA, complete cds.
5019	CVD	AA	AT	TT	D00510	Homo sapiens mRNA for calphobindin II, complete cds.
5165	ADR3	CC	AC	AA	M21574	Human platelet-derived growth factor receptor alpha (PDGFRA) mRNA, complete cds.
5165	ADR5	CC	AC	AA	M21574	Human platelet-derived growth factor receptor alpha (PDGFRA) mRNA, complete cds.
5165	ADR	CC	AC	AA	M21574	Human platelet-derived growth factor receptor alpha (PDGFRA) mRNA, complete cds.
5278	ADR5	GG	AG	AA	D87812	Human mRNA for carnitine palmitoyltransferase I, complete cds.
5287	VEFF	CC	CT	TT	J02611	Human apolipoprotein D mRNA, complete cds.
5320	CVD	AA	AG	GG	J03799	Human colin carcinoma laminin-binding protein mRNA, complete cds.
5324	VEFF	TT	CT	CC	J04046	Human calmodulin mRNA, complete cds.
5373	ADR5	GG	GT	TT	L06237	Human microtubule-associated protein 1B (MAP1B) gene, complete cds.
5375	ADR5	CC	CT	TT	L06237	Human microtubule-associated protein 1B (MAP1B) gene, complete cds.
5376	ADR5	AA	AT	null	L06237	Human microtubule-associated protein 1B (MAP1B) gene, complete cds.
5377	ADR	TT	CT	CC	L06237	Human microtubule-associated protein 1B (MAP1B) gene, complete cds.
5377	ADR5	TT	CT	CC	L06237	Human microtubule-associated protein 1B (MAP1B) gene, complete cds.
5517	ADR	AA	AG	GG	AA609457	PYRUVATE DEHYDROGENASE KINASE.
5518	ADR5	GG	CG	CC	AA609457	PYRUVATE DEHYDROGENASE KINASE.
5564	CVD	GG	GT	TT	M14584	Human interleukin 6 mRNA, complete cds.
5569	ADR5	GG	AG	AA	M14745	Human bcl-2 mRNA.
5716	ADR3	GG	CG	CC	AL008637	Human DNA sequence from clone CTA-833B7 on chromosome 22q12.3-13.2 Contains the NCF4 gene for cytosolic neutrophil factor 4 (40kD), the 5' part of the CSF2RB gene for granulocyte-macrophage low-affinity colony stimulating factor 2 receptor beta, ESTs, STS
5716	ADR5	GG	CG	CC	AL008637	Human DNA sequence from clone CTA-833B7 on chromosome 22q12.3-13.2 Contains the

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
						NCF4 gene for cytosolic neutrophil factor 4 (40kD), the 5` part of the CSF2RB gene for granulocyte-macrophage low-affinity colony stimulating factor 2 receptor beta, ESTs, STS
5717	ADR5	GG	AG	AA	AL008637	Human DNA sequence from clone CTA-833B7 on chromosome 22q12.3-13.2 Contains the NCF4 gene for cytosolic neutrophil factor 4 (40kD), the 5` part of the CSF2RB gene for granulocyte-macrophage low-affinity colony stimulating factor 2 receptor beta, ESTs, STS
5717	CVD	GG	AG	AA	AL008637	Human DNA sequence from clone CTA-833B7 on chromosome 22q12.3-13.2 Contains the NCF4 gene for cytosolic neutrophil factor 4 (40kD), the 5` part of the CSF2RB gene for granulocyte-macrophage low-affinity colony stimulating factor 2 receptor beta, ESTs, STS
5850	CVD	GG	AG	AA	M95724	H.sapiens centromere autoantigen C (CENPC) mRNA, complete cds.
5959	CVD	GG	AG	AA	U12789	Human clone HSH1 HMG CoA synthase mRNA, partial cds.
6151	ADR	CC	AC	AA	U49245	Human geranylgeranyl transferase type II beta-subunit mRNA, complete cds.
6236	ADR	TT	CT	CC	NM_000436	Homo sapiens 3-oxoacid CoA transferase (OXCT), nuclear gene encoding mitochondrial protein, mRNA
6277	ADR5	TT	GT	GG	NM_003477	Homo sapiens Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein (PDX1), mRNA
6277	ADR	TT	GT	GG	NM_003477	Homo sapiens Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein (PDX1), mRNA
6277	ADR3	TT	GT	GG	NM_003477	Homo sapiens Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein (PDX1), mRNA
6313	UEFF	CC	CT	TT	X05199	Human mRNA for plasminogen
6369	CVD	TT	CT	CC	X52011	H.sapiens MYF6 gene encoding a muscle determination factor
6374	ADR3	TT	CT	CC	X52022	H.sapiens RNA for type VI collagen alpha3 chain
6396	CVD	TT	CT	CC	X54807	Human CYP2C8 gene for cytochrome P-450, 5` flank and exon 1
6486	CVD	GG	AG	AA	X69086	H.sapiens mRNA for utrophin

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
6520	ADR5	GG	AG	AA	X76930	H.sapiens HNF4 mRNA for hepatocyte nuclear factor 4
6520	ADR3	GG	AG	AA	X76930	H.sapiens HNF4 mRNA for hepatocyte nuclear factor 4
6520	ADR	GG	AG	AA	X76930	H.sapiens HNF4 mRNA for hepatocyte nuclear factor 4
6522	ADR3	GG	AG	AA	X76930	H.sapiens HNF4 mRNA for hepatocyte nuclear factor 4
6522	ADR	GG	AG	AA	X76930	H.sapiens HNF4 mRNA for hepatocyte nuclear factor 4
6524	ADR3	AA	AG	GG	X76930	H.sapiens HNF4 mRNA for hepatocyte nuclear factor 4
6596	ADR3	CC	CT	TT	X98330	H.sapiens mRNA for ryanodine receptor 2
6596	ADR5	CC	CT	TT	X98330	H.sapiens mRNA for ryanodine receptor 2
6596	ADR	CC	CT	TT	X98330	H.sapiens mRNA for ryanodine receptor 2
6734	CVD	AA	AC	CC	AC002543	Homo sapiens BAC clone CTA-300C3 from 7q31.2, complete sequence.
6743	ADR	GG	CG	CC	X00568	Human mRNA for lipoprotein apoCII
7128	ADR3	CC	CT	TT	J05096	Human Na,K-ATPase subunit alpha 2 (ATP1A2) gene, complete cds.
7128	ADR5	CC	CT	TT	J05096	Human Na,K-ATPase subunit alpha 2 (ATP1A2) gene, complete cds.
7128	ADR	CC	CT	TT	J05096	Human Na,K-ATPase subunit alpha 2 (ATP1A2) gene, complete cds.
7363	CVD	GG	AG	AA	M15887	Human endozepine (putative ligand of benzodiazepine receptor) mRNA, complete cds.
7409	ADR5	AA	AG	GG	M33519	Human HLA-B-associated transcript 3 (BAT3) mRNA, complete cds.
7409	ADR3	AA	AG	GG	M33519	Human HLA-B-associated transcript 3 (BAT3) mRNA, complete cds.
8138	CVD	TT	CT	CC	AC002457	Homo sapiens BAC clone CTB-60P12 from 7q21, complete sequence.
8168	CVD	CC	AC	AA	AF019742	Homo sapiens caveolin gene, promoter region and partial cds.
8210	ADR3	GG	AG	AA	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
8210	ADR	GG	AG	AA	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
8241	CVD	AA	AG	GG	AF165281	Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds.
8249	ADR3	CC	CT	TT	AF185589	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region.

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
8249	ADR5	CC	CT	TT	AF185589	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region.
8480	CVD	CC	CG	GG	U63415	Human peroxisome proliferator activated receptor gamma 2 mRNA, complete cds.
8577	ADR3	TT	CT	CC	M21616	Human platelet-derived growth factor (PDGF) receptor mRNA, complete cds.
8577	ADR	TT	CT	CC	M21616	Human platelet-derived growth factor (PDGF) receptor mRNA, complete cds.
8577	ADR5	TT	CT	CC	M21616	Human platelet-derived growth factor (PDGF) receptor mRNA, complete cds.
8578	ADR3	GG	AG	AA	M21616	Human platelet-derived growth factor (PDGF) receptor mRNA, complete cds.
8653	ADR	CC	CT	TT	L06237	Human microtubule-associated protein 1B (MAP1B) gene, complete cds.
8653	ADR3	CC	CT	TT	L06237	Human microtubule-associated protein 1B (MAP1B) gene, complete cds.
8653	ADR5	CC	CT	TT	L06237	Human microtubule-associated protein 1B (MAP1B) gene, complete cds.
8816	CVD	GG	CG	CC	L36033	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds.
8931	ADR3	CC	CT	TT	M14780	Human creatine kinase M mRNA, complete cds.
8943	ADR3	AA	AC	CC	AF050163	Homo sapiens lipoprotein lipase precursor, gene, partial cds.
9243	VEFF	CC	CG	GG	AB055890	Homo sapiens c-lbc mRNA for guanine nucleotide exchange factor Lbc, complete cds.
9243	ADR5	CC	CG	GG	AB055890	Homo sapiens c-lbc mRNA for guanine nucleotide exchange factor Lbc, complete cds.
9243	UEFF	CC	CG	GG	AB055890	Homo sapiens c-lbc mRNA for guanine nucleotide exchange factor Lbc, complete cds.
9523	ADR5	GG	AG	AA	U17195	Homo sapiens A-kinase anchor protein (AKAP100) mRNA, complete cds.
9940	CVD	CC	CT	TT	X54807	Human CYP2C8 gene for cytochrome P-450, 5' flank and exon 1
10091	ADR3	TT	CT	CC	NM_005015	Homo sapiens oxidase (cytochrome c) assembly 1-like (OXA1L), mRNA
10541	UEFF	GG	CG	CC	AF066859	Homo sapiens muscle glycogen phosphorylase (PYGM) mRNA, complete cds.
10541	VEFF	GG	CG	CC	AF066859	Homo sapiens muscle glycogen phosphorylase (PYGM) mRNA, complete cds.
10600	CVD	GG	AG	AA	AF129756	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds.

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
10745	CVD	GG	AG	AA	D11456	Human mRNA for Xanthine dehydrogenase, complete cds.
10748	CVD	TT	CT	CC	D11456	Human mRNA for Xanthine dehydrogenase, complete cds.
10749	CVD	CC	CG	GG	D11456	Human mRNA for Xanthine dehydrogenase, complete cds.
10785	CVD	TT	CT	CC	D50678	Human mRNA for apolipoprotein E receptor 2, complete cds.
10811	CVD	AA	AG	GG	D86425	Homo sapiens mRNA for osteonidogen, complete cds.
10830	CVD	GG	AG	AA	J02610	Human apolipoprotein B-100 mRNA, complete cds.
10949	VEFF	GG	CG	CC	M10065	Human apolipoprotein E (epsilon-4 allele) gene, complete cds.
10949	EFF	GG	CG	CC	M10065	Human apolipoprotein E (epsilon-4 allele) gene, complete cds.
10962	CVD	AA	AG	GG	M18079	Human, intestinal fatty acid binding protein gene, complete cds, and an Alu repetitive element.
10962	ADR3	AA	AG	GG	M18079	Human, intestinal fatty acid binding protein gene, complete cds, and an Alu repetitive element.
10966	ADR3	TT	CT	CC	M18079	Human, intestinal fatty acid binding protein gene, complete cds, and an Alu repetitive element.
10966	ADR5	TT	CT	CC	M18079	Human, intestinal fatty acid binding protein gene, complete cds, and an Alu repetitive element.
11000	CVD	TT	CT	CC	M34424	Human acid alpha-glucosidase (GAA) mRNA, complete cds.
11000	ADR3	TT	CT	CC	M34424	Human acid alpha-glucosidase (GAA) mRNA, complete cds.
11000	ADR5	TT	CT	CC	M34424	Human acid alpha-glucosidase (GAA) mRNA, complete cds.
11001	CVD	TT	CT	CC	M34424	Human acid alpha-glucosidase (GAA) mRNA, complete cds.
11001	ADR3	TT	CT	CC	M34424	Human acid alpha-glucosidase (GAA) mRNA, complete cds.
11020	ADR3	CC	CT	TT	M60092	Human myoadenylate deaminase (AMPD1) mRNA, complete cds.
11073	CVD	GG	CG	CC	AF070670	Homo sapiens protein phosphatase 2C alpha 2 mRNA, complete cds.

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
11192	ADR5	TT	AT	AA	NM_003477	Homo sapiens Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein (PDX1), mRNA
11192	ADR3	TT	AT	AA	NM_003477	Homo sapiens Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein (PDX1), mRNA
11248	ADR3	CC	CT	TT	X60435	H.sapiens gene PACAP for pituitary adenylate cyclase activating polypeptide
11248	ADR	CC	CT	TT	X60435	H.sapiens gene PACAP for pituitary adenylate cyclase activating polypeptide
11410	VEFF	GG	GT	TT	AC004590	ABCC3: ATP-binding cassette, sub-family C (CFTR/MRP), member 3
11448	CVD	GG	AG	AA	AF050163	Homo sapiens lipoprotein lipase precursor, gene, partial cds.
11448	ADR	GG	AG	AA	AF050163	Homo sapiens lipoprotein lipase precursor, gene, partial cds.
11450	CVD	TT	AT	AA	AF050163	Homo sapiens lipoprotein lipase precursor, gene, partial cds.
11456	CVD	AA	AG	GG	AF051427	Homo sapiens estrogen receptor beta mRNA, complete cds.
11462	CVD	GG	GT	TT	AF051427	Homo sapiens estrogen receptor beta mRNA, complete cds.
11483	ADR5	TT	CT	CC	L19592	Homo sapiens interleukin 8 receptor alpha (IL8RA) gene, complete cds.
11483	ADR3	TT	CT	CC	L19592	Homo sapiens interleukin 8 receptor alpha (IL8RA) gene, complete cds.
11483	ADR	TT	CT	CC	L19592	Homo sapiens interleukin 8 receptor alpha (IL8RA) gene, complete cds.
11531	CVD	GG	AG	AA	X52773	Human mRNA for retinoic acid receptor-like protein
11536	CVD	CC	CG	GG	AL022721	Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferato
11537	ADR	AA	AG	GG	AL022721	Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
						Proliferator delta
11558	CVD	AA	AC	CC	AC006312	Homo sapiens chromosome 9, clone hRPK.401_G_18, complete sequence.
11585	CVD	GG	GT	TT	AC073593	Homo sapiens 12 BAC RP11-13J12 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
11594	ADR3	TT	CT	CC	AF026069	Homo sapiens phosphomevalonate kinase (HUMPMKI) gene, partial cds.
11594	ADR	TT	CT	CC	AF026069	Homo sapiens phosphomevalonate kinase (HUMPMKI) gene, partial cds.
11614	CVD	TT	CT	CC	AF107885	Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes.
11631	ADR5	GG	AG	AA	AL022721	Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator delta
11631	ADR3	GG	AG	AA	AL022721	Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator delta
11637	CVD	AA	AC	CC	M19154	Human transforming growth factor-beta-2 mRNA, complete cds.
11641	ADR	GG	CG	CC	U12788	Human HMG CoA synthase mRNA, partial cds.
11645	CVD	GG	AG	AA	X05839	Human transforming growth factor-beta precursor gene exon 1 and 5`flanking region (and joined CDS)
11646	CVD	CC	CT	TT	X05839	Human transforming growth factor-beta precursor gene exon 1 and 5`flanking region (and joined CDS)
11652	CVD	CC	CT	TT	AH002776	Human low density lipoprotein receptor gene
11727	ADR5	GG	AG	AA	AB043943	Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
11727	ADR3	GG	AG	AA	AB043943	Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.
11728	ADR5	TT	CT	CC	AB043943	Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.
11914	ADR3	AA	AT	TT	AF030555	Homo sapiens acyl-CoA synthetase 4 (ACS4) mRNA, complete cds.
11938	ADR3	TT	CT	CC	AF058921	Homo sapiens cytosolic phospholipase A2-gamma mRNA, complete cds.
11938	ADR5	TT	CT	CC	AF058921	Homo sapiens cytosolic phospholipase A2-gamma mRNA, complete cds.
11950	ADR5	GG	AG	AA	AF080222	Homo sapiens thrombin-activable fibrinolysis inhibitor gene, 5`-flanking region.
11950	ADR3	GG	AG	AA	AF080222	Homo sapiens thrombin-activable fibrinolysis inhibitor gene, 5`-flanking region.
11950	ADR	GG	AG	AA	AF080222	Homo sapiens thrombin-activable fibrinolysis inhibitor gene, 5`-flanking region.
11951	ADR5	GG	AG	AA	AF080222	Homo sapiens thrombin-activable fibrinolysis inhibitor gene, 5`-flanking region.
11951	UEFF	GG	AG	AA	AF080222	Homo sapiens thrombin-activable fibrinolysis inhibitor gene, 5`-flanking region.
12008	ADR	CC	CT	null	AF107885	Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes.
12031	ADR3	AA	AG	GG	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
12031	ADR5	AA	AG	GG	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
12031	ADR	AA	AG	GG	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
12032	UEFF	TT	CT	CC	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
12032	ADR	TT	CT	CC	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
12032	VEFF	TT	CT	CC	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
12148	ADR5	GG	AG	AA	AL022721	Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator delta
12148	ADR	GG	AG	AA	AL022721	Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
						alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator delta
12148	ADR3	GG	AG	AA	AL022721	Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator delta
12207	ADR5	AA	AG	GG	D11456	Human mRNA for Xanthine dehydrogenase, complete cds.
12207	ADR	AA	AG	GG	D11456	Human mRNA for Xanthine dehydrogenase, complete cds.
12207	ADR3	AA	AG	GG	D11456	Human mRNA for Xanthine dehydrogenase, complete cds.
12399	ADR5	AA	AG	GG	D86982	Human mRNA for KIAA0229 gene, partial cds.
12399	ADR3	AA	AG	GG	D86982	Human mRNA for KIAA0229 gene, partial cds.
12399	ADR	AA	AG	GG	D86982	Human mRNA for KIAA0229 gene, partial cds.
12554	ADR	AA	AT	TT	HSVDAC1X	Human voltage-dependent anion channel isoform 1 (VDAC) mRNA, complete cds.
12554	VEFF	AA	AT	TT	HSVDAC1X	Human voltage-dependent anion channel isoform 1 (VDAC) mRNA, complete cds.
12851	ADR5	TT	CT	CC	M33336	Human cAMP-dependent protein kinase type I-alpha subunit (PRKAR1A) mRNA, complete cds.
12851	ADR	TT	CT	CC	M33336	Human cAMP-dependent protein kinase type I-alpha subunit (PRKAR1A) mRNA, complete cds.
13025	ADR3	AA	AC	CC	M85168	Human glycogen debranching enzyme mRNA, complete cds.
13025	ADR5	AA	AC	CC	M85168	Human glycogen debranching enzyme mRNA, complete cds.
13191	CVD	GG	AG	AA	U12789	Human clone HSH1 HMG CoA synthase mRNA, partial cds.
13192	ADR3	TT	CT	CC	U12789	Human clone HSH1 HMG CoA synthase mRNA, partial cds.
13192	ADR5	TT	CT	CC	U12789	Human clone HSH1 HMG CoA synthase mRNA, partial cds.
13192	ADR	TT	CT	CC	U12789	Human clone HSH1 HMG CoA synthase mRNA, partial cds.

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
13193	ADR3	GG	AG	AA	U12789	Human clone HSH1 HMG CoA synthase mRNA, partial cds.
13193	ADR5	GG	AG	AA	U12789	Human clone HSH1 HMG CoA synthase mRNA, partial cds.
13338	UEFF	GG	AG	AA	U46023	Human Xq28 mRNA, complete cds.
13338	VEFF	GG	AG	AA	U46023	Human Xq28 mRNA, complete cds.
13339	ADR	GG	AG	AA	U46023	Human Xq28 mRNA, complete cds.
13339	CVD	GG	AG	AA	U46023	Human Xq28 mRNA, complete cds.
13340	VEFF	CC	AC	AA	U46023	Human Xq28 mRNA, complete cds.
13479	UEFF	GG	AG	AA	U95626	Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.
13633	ADR3	TT	CT	CC	HSGKTS1	H.sapiens mRNA for glycerol kinase testis specific 1.
13633	ADR	TT	CT	CC	HSGKTS1	H.sapiens mRNA for glycerol kinase testis specific 1.
13929	ADR5	GG	AG	AA	L28101	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds.
14065	EFF	CC	CT	TT	AC006022	Homo sapiens PAC clone RP5-1131G17 from 7p15.1-p14, complete sequence.
14083	ADR	TT	CT	CC	AF044953	Homo sapiens NADH:ubiquinone oxidoreductase PGIV subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.
14085	EFF	TT	CT	CC	AF044954	Homo sapiens NADH:ubiquinone oxidoreductase PDSW subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.
14087	EFF	TT	CT	CC	AF044954	Homo sapiens NADH:ubiquinone oxidoreductase PDSW subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.
14102	ADR5	CC	CT	TT	AF087661	Homo sapiens NADH-ubiquinone oxidoreductase 42 kDa subunit mRNA, complete cds, nuclear gene encoding mitochondrial protein.
14102	EFF	CC	CT	TT	AF087661	Homo sapiens NADH-ubiquinone oxidoreductase 42 kDa subunit mRNA, complete cds, nuclear gene encoding mitochondrial protein.

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
14103	EFF	CC	CT	TT	AF087661	Homo sapiens NADH-ubiquinone oxidoreductase 42 kDa subunit mRNA, complete cds, nuclear gene encoding mitochondrial protein.
14103	VEFF	CC	CT	TT	AF087661	Homo sapiens NADH-ubiquinone oxidoreductase 42 kDa subunit mRNA, complete cds, nuclear gene encoding mitochondrial protein.
14103	UEFF	CC	CT	TT	AF087661	Homo sapiens NADH-ubiquinone oxidoreductase 42 kDa subunit mRNA, complete cds, nuclear gene encoding mitochondrial protein.
14129	ADR3	AA	AG	GG	BC003093	Homo sapiens, Rab geranylgeranyltransferase, alpha subunit, clone MGC:1485 IMAGE:3537388, mRNA, complete cds.
14326	EFF	AA	AC	CC	NM_005390	Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2), mRNA
14503	ADR5	CC	CT	TT	AJ276178	Homo sapiens partial ZNF202 gene for zinc finger protein homolog, exon 2
14503	ADR3	CC	CT	TT	AJ276178	Homo sapiens partial ZNF202 gene for zinc finger protein homolog, exon 2
14537	ADR	CC	CT	TT	U22526	Human 2,3-oxidosqualene-lanosterol cyclase mRNA, complete cds.
15915	ADR	TT	CT	CC	L32179	Human arylacetamide deacetylase mRNA, complete cds.
15915	ADR3	TT	CT	CC	L32179	Human arylacetamide deacetylase mRNA, complete cds.
19289	CVD	GG	AG	AA	AL031651	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM2)
36958	ADR3	CC	CG	GG	AF050163	Homo sapiens lipoprotein lipase precursor, gene, partial cds.
37158	ADR	CC	AC	AA	D63807	Human mRNA for lanosterol synthase, complete cds.
37160	UEFF	CC	CT	TT	D63807	Human mRNA for lanosterol synthase, complete cds.
37412	ADR5	TT	GT	GG	M74775	Human lysosomal acid lipase/cholesteryl esterase mRNA, complete cds.
37412	ADR3	TT	GT	GG	M74775	Human lysosomal acid lipase/cholesteryl esterase mRNA, complete cds.
37457	CVD	TT	AT	AA	S67973	NDUFV1=NADH:ubiquinone oxidoreductase flavoprotein 1 subunit [human, kidney, mRNA Partial, 771 nt].
37704	ADR5	CC	CT	null	XM_010049	Homo sapiens peroxisome proliferative activated receptor, alpha (PPARA), mRNA.

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
38959	CVD	CC	AC	AA	AL133392	Human DNA sequence from clone CITF22-45C1 on chromosome 22 Contains the 3` part of the CSF2RB gene for low-affinity granulocyte-macrophage colony stimulating factor 2 receptor beta, the CSF2RB2 gene for colony stimulating factor 2 receptor beta 2, ESTs, STS
38959	EFF	CC	AC	AA	AL133392	Human DNA sequence from clone CITF22-45C1 on chromosome 22 Contains the 3` part of the CSF2RB gene for low-affinity granulocyte-macrophage colony stimulating factor 2 receptor beta, the CSF2RB2 gene for colony stimulating factor 2 receptor beta 2, ESTs, STS
39292	ADR5	GG	AG	AA	M33388	Human cytochrome P450 IID6 (CYP2D6) gene, complete cds.
39698	ADR3	TT	CT	CC	X07619	Human mRNA for cytochrome P450 db1 variant b
39756	ADR3	TT	CT	CC	X58468	Human CYP2D7BP pseudogene for cytochrome P450 2D6
39951	ADR	TT	CT	CC	AF005896	Homo sapiens Na K-ATPase beta-3 subunit (atp1b3) gene, exon 7 and complete cds.
39951	ADR5	TT	CT	CC	AF005896	Homo sapiens Na K-ATPase beta-3 subunit (atp1b3) gene, exon 7 and complete cds.
40466	EFF	GG	GT	TT	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
40466	UEFF	GG	GT	TT	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
40466	VEFF	GG	GT	TT	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
44442	ADR5	AA	AG	GG	NM_001931	Homo sapiens dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) (DLAT), mRNA
55504	ADR	TT	CT	CC	SECONDARY: NM_000191	SECONDARY TO Homo sapiens 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria) (HMGCL), mRNA
55542	ADR	CC	AC	AA	SECONDARY: NM_000191	SECONDARY TO Homo sapiens 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria) (HMGCL), mRNA
55670	VEFF	CC	CT	TT	SECONDARY: NM_001876	SECONDARY TO Homo sapiens carnitine palmitoyltransferase I, liver (CPT1A), nuclear gene encoding mitochondrial protein, mRNA
55736	ADR5	AA	AG	GG	SECONDARY: M23234	SECONDARY TO ABCB4

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
55748	ADR5	TT	CT	CC	SECONDARY: M23234	SECONDARY TO ABCB4
55813	ADR3	TT	CT	CC	SECONDARY: M34551	SECONDARY TO Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.
55845	VEFF	CC	AC	AA	SECONDARY: M34551	SECONDARY TO Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.
55845	ADR3	CC	AC	AA	SECONDARY: M34551	SECONDARY TO Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.
55845	UEFF	CC	AC	AA	SECONDARY: M34551	SECONDARY TO Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.
55923	ADR	CC	CT	TT	SECONDARY: M95724	SECONDARY TO H.sapiens centromere autoantigen C (CENPC) mRNA, complete cds.
55923	ADR3	CC	CT	TT	SECONDARY: M95724	SECONDARY TO H.sapiens centromere autoantigen C (CENPC) mRNA, complete cds.
55945	ADR	GG	AG	AA	SECONDARY: M95724	SECONDARY TO H.sapiens centromere autoantigen C (CENPC) mRNA, complete cds.
55945	ADR3	GG	AG	AA	SECONDARY: M95724	SECONDARY TO H.sapiens centromere autoantigen C (CENPC) mRNA, complete cds.
56007	ADR3	TT	CT	CC	SECONDARY: NM_001303	SECONDARY TO Homo sapiens COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast) (COX10), nuclear gene encoding mitochondrial protein, mRNA
56007	ADR5	TT	CT	CC	SECONDARY: NM_001303	SECONDARY TO Homo sapiens COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast) (COX10), nuclear gene encoding mitochondrial protein, mRNA

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
56011	ADR5	AA	AG	null	SECONDARY: NM_001303	SECONDARY TO Homo sapiens COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast) (COX10), nuclear gene encoding mitochondrial protein, mRNA
56104	UEFF	GG	AG	AA	SECONDARY: AF091582	SECONDARY TO ABCB11
56113	ADR5	GG	GT	TT	SECONDARY: AF091582	SECONDARY TO ABCB11
56113	ADR3	GG	GT	TT	SECONDARY: AF091582	SECONDARY TO ABCB11
56636	ADR	TT	CT	CC	SECONDARY: L13972	SECONDARY TO Homo sapiens beta-galactoside alpha-2,3-sialyltransferase (SIAT4A) mRNA, complete cds.
56636	ADR3	TT	CT	CC	SECONDARY: L13972	SECONDARY TO Homo sapiens beta-galactoside alpha-2,3-sialyltransferase (SIAT4A) mRNA, complete cds.
56636	ADR5	TT	CT	CC	SECONDARY: L13972	SECONDARY TO Homo sapiens beta-galactoside alpha-2,3-sialyltransferase (SIAT4A) mRNA, complete cds.
56666	ADR3	GG	AG	AA	SECONDARY: AF027406	SECONDARY TO Homo sapiens muscle-specific serine kinase 1 (MSSK1) mRNA, complete cds.
56666	ADR5	GG	AG	AA	SECONDARY: AF027406	SECONDARY TO Homo sapiens muscle-specific serine kinase 1 (MSSK1) mRNA, complete cds.
56666	ADR	GG	AG	AA	SECONDARY: AF027406	SECONDARY TO Homo sapiens muscle-specific serine kinase 1 (MSSK1) mRNA, complete cds.
56667	EFF	TT	CT	CC	AF027406	Homo sapiens muscle-specific serine kinase 1 (MSSK1) mRNA, complete cds.
56667	ADR3	TT	CT	CC	AF027406	Homo sapiens muscle-specific serine kinase 1 (MSSK1) mRNA, complete cds.
56780	ADR3	GG	AG	AA	SECONDARY:	SECONDARY TO Homo sapiens, ATPase, Na+/K+ transporting, beta 1 polypeptide

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
					BC000006	
56780	ADR	GG	AG	AA	SECONDARY: BC000006	SECONDARY TO Homo sapiens, ATPase, Na+/K+ transporting, beta 1 polypeptide
56876	UEFF	TT	CT	CC	SECONDARY: AF066859	SECONDARY TO Homo sapiens muscle glycogen phosphorylase (PYGM) mRNA, complete cds.
56876	EFF	TT	CT	CC	SECONDARY: AF066859	SECONDARY TO Homo sapiens muscle glycogen phosphorylase (PYGM) mRNA, complete cds.
56876	VEFF	TT	CT	CC	SECONDARY: AF066859	SECONDARY TO Homo sapiens muscle glycogen phosphorylase (PYGM) mRNA, complete cds.
56978	ADR5	AA	AG	GG	SECONDARY: D11456	SECONDARY TO Human mRNA for Xanthine dehydrogenase, complete cds.
57000	VEFF	AA	AT	TT	SECONDARY: D11456	SECONDARY TO Human mRNA for Xanthine dehydrogenase, complete cds.
57000	UEFF	AA	AT	TT	SECONDARY: D11456	SECONDARY TO Human mRNA for Xanthine dehydrogenase, complete cds.
57000	CVD	AA	AT	TT	SECONDARY: D11456	SECONDARY TO Human mRNA for Xanthine dehydrogenase, complete cds.
57313	UEFF	TT	CT	CC	SECONDARY: AB014460	SECONDARY TO Homo sapiens TSC2, NTHL1/NTH1 and SLC9A3R2/E3KARP genes, partial and complete cds.
57734	ADR3	CC	CG	GG	SECONDARY: AL022721	SECONDARY TO Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator delta
57837	ADR3	AA	AG	GG	SECONDARY:	SECONDARY TO Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
					AB043943	
57853	EFF	TT	CT	CC	SECONDARY: AB043943	SECONDARY TO Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.
57853	UEFF	TT	CT	CC	SECONDARY: AB043943	SECONDARY TO Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.
57853	VEFF	TT	CT	CC	SECONDARY: AB043943	SECONDARY TO Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.
57854	EFF	GG	AG	AA	SECONDARY: AB043943	SECONDARY TO Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.
57854	UEFF	GG	AG	AA	SECONDARY: AB043943	SECONDARY TO Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.
57854	ADR3	GG	AG	AA	SECONDARY: AB043943	SECONDARY TO Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.
58295	ADR	AA	AG	GG	SECONDARY: X83618	SECONDARY TO H.sapiens mRNA for 3-hydroxy-3-methylglutaryl coenzyme A synthase
58402	ADR3	TT	CT	CC	SECONDARY: U46023	SECONDARY TO Human Xq28 mRNA, complete cds.
58407	VEFF	GG	GT	TT	SECONDARY: U46023	SECONDARY TO Human Xq28 mRNA, complete cds.
58407	UEFF	GG	GT	TT	SECONDARY: U46023	SECONDARY TO Human Xq28 mRNA, complete cds.
58440	UEFF	TT	CT	CC	SECONDARY: U46023	SECONDARY TO Human Xq28 mRNA, complete cds.
58525	ADR	CC	CT	TT	SECONDARY:	SECONDARY TO Homo sapiens putative N6-DNA-methyltransferase (N6AMT1), mRNA

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
					NM_013240	
58525	ADR3	CC	CT	TT	SECONDARY: NM_013240	SECONDARY TO Homo sapiens putative N6-DNA-methyltransferase (N6AMT1), mRNA
58525	ADR5	CC	CT	TT	SECONDARY: NM_013240	SECONDARY TO Homo sapiens putative N6-DNA-methyltransferase (N6AMT1), mRNA
58533	ADR	CC	CT	TT	SECONDARY: NM_013240	SECONDARY TO Homo sapiens putative N6-DNA-methyltransferase (N6AMT1), mRNA
58533	ADR3	CC	CT	TT	SECONDARY: NM_013240	SECONDARY TO Homo sapiens putative N6-DNA-methyltransferase (N6AMT1), mRNA
58533	ADR5	CC	CT	TT	SECONDARY: NM_013240	SECONDARY TO Homo sapiens putative N6-DNA-methyltransferase (N6AMT1), mRNA
58544	ADR5	GG	AG	AA	SECONDARY: NM_013240	SECONDARY TO Homo sapiens putative N6-DNA-methyltransferase (N6AMT1), mRNA
58716	ADR3	TT	CT	CC	SECONDARY: BC002772	SECONDARY TO Homo sapiens, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (14kD, B14), clone MGC:3686 IMAGE:3619356, mRNA, complete cds.
58716	ADR5	TT	CT	CC	SECONDARY: BC002772	SECONDARY TO Homo sapiens, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (14kD, B14), clone MGC:3686 IMAGE:3619356, mRNA, complete cds.
58736	EFF	CC	CT	TT	SECONDARY: BC002772	SECONDARY TO Homo sapiens, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (14kD, B14), clone MGC:3686 IMAGE:3619356, mRNA, complete cds.
58808	ADR	AA	AG	GG	SECONDARY: NM_003889	SECONDARY TO nuclear hormone receptor PRR2
58809	ADR5	CC	AC	AA	SECONDARY: NM_003889	SECONDARY TO nuclear hormone receptor PRR2
58809	ADR3	CC	AC	AA	SECONDARY:	SECONDARY TO nuclear hormone receptor PRR2

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
					NM_003889	
58809	UEFF	CC	AC	AA	SECONDARY: NM_003889	SECONDARY TO nuclear hormone receptor PRR2
58886	ADR3	AA	AG	GG	SECONDARY: AL008637	SECONDARY TO Human DNA sequence from clone CTA-833B7 on chromosome 22q12.3-13.2 Contains the NCF4 gene for cytosolic neutrophil factor 4 (40kD), the 5` part of the CSF2RB gene for granulocyte-macrophage low-affinity colony stimulating factor 2 receptor beta
58886	ADR5	AA	AG	GG	SECONDARY: AL008637	SECONDARY TO Human DNA sequence from clone CTA-833B7 on chromosome 22q12.3-13.2 Contains the NCF4 gene for cytosolic neutrophil factor 4 (40kD), the 5` part of the CSF2RB gene for granulocyte-macrophage low-affinity colony stimulating factor 2 receptor beta
58926	ADR3	CC	CT	TT	SECONDARY: L78810	SECONDARY TO Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.
58926	ADR5	CC	CT	TT	SECONDARY: L78810	SECONDARY TO Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.
58926	CVD	CC	CT	TT	SECONDARY: L78810	SECONDARY TO Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.
58968	ADR5	AA	AG	GG	SECONDARY: L78810	SECONDARY TO Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.
58968	ADR3	AA	AG	GG	SECONDARY: L78810	SECONDARY TO Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.
58985	ADR5	GG	AG	AA	SECONDARY: L78810	SECONDARY TO Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.
59113	ADR5	CC	CG	GG	SECONDARY:	SECONDARY TO Homo sapiens acyl-CoA synthetase 4 (ACS4) mRNA, complete cds.

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
					AF030555	
59113	ADR3	CC	CG	GG	SECONDARY: AF030555	SECONDARY TO Homo sapiens acyl-CoA synthetase 4 (ACS4) mRNA, complete cds.
59236	ADR	GG	AG	AA	SECONDARY: NM_002340	SECONDARY TO Homo sapiens lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) (LSS), mRNA
59236	ADR3	GG	AG	AA	SECONDARY: NM_002340	SECONDARY TO Homo sapiens lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) (LSS), mRNA
59237	VEFF	CC	CT	TT	SECONDARY: NM_002340	SECONDARY TO Homo sapiens lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) (LSS), mRNA
59237	EFF	CC	CT	TT	SECONDARY: NM_002340	SECONDARY TO Homo sapiens lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) (LSS), mRNA
59267	UEFF	TT	CT	CC	SECONDARY: NM_002340	SECONDARY TO Homo sapiens lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) (LSS), mRNA
59352	ADR	TT	CT	CC	SECONDARY: M34960	SECONDARY TO Homo sapiens transcription factor IID mRNA, complete cds.
59363	CVD	TT	CT	CC	SECONDARY: M34960	SECONDARY TO Homo sapiens transcription factor IID mRNA, complete cds.
59368	ADR	TT	CT	CC	SECONDARY: M34960	SECONDARY TO Homo sapiens transcription factor IID mRNA, complete cds.
59371	VEFF	CC	CT	TT	SECONDARY: M34960	SECONDARY TO Homo sapiens transcription factor IID mRNA, complete cds.
59371	UEFF	CC	CT	TT	SECONDARY: M34960	SECONDARY TO Homo sapiens transcription factor IID mRNA, complete cds.
59372	ADR	CC	CT	TT	SECONDARY:	SECONDARY TO Homo sapiens transcription factor IID mRNA, complete cds.

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
					M34960	
59372	ADR3	CC	CT	TT	SECONDARY: M34960	SECONDARY TO Homo sapiens transcription factor IID mRNA, complete cds.
59443	ADR5	TT	CT	CC	SECONDARY: U84007	SECONDARY TO Human glycogen debranching enzyme isoform 1 (AGL) mRNA, alternatively spliced isoform, complete cds.
900080	ADR3	GG	CG	CC	NM_013240	Homo sapiens putative N6-DNA-methyltransferase (N6AMT1), mRNA
900080	ADR5	GG	CG	CC	NM_013240	Homo sapiens putative N6-DNA-methyltransferase (N6AMT1), mRNA
900102	UEFF	TT	GT	GG	NM_003889	nuclear hormone receptor PRR2
900102	VEFF	TT	GT	GG	NM_003889	nuclear hormone receptor PRR2
900111	UEFF	GG	AG	AA	NM_003889	nuclear hormone receptor PRR2
900111	VEFF	GG	AG	AA	NM_003889	nuclear hormone receptor PRR2
900117	CVD	TT	GT	GG	AF050163	Homo sapiens lipoprotein lipase precursor, gene, partial cds.
900118	EFF	GG	AG	AA	U46024	MTM1: myotubular myopathy 1
900118	VEFF	GG	AG	AA	U46024	MTM1: myotubular myopathy 1
900118	ADR5	GG	AG	AA	U46024	MTM1: myotubular myopathy 1
900120	EFF	TT	CT	CC	U46024	MTM1: myotubular myopathy 1
900121	EFF	TT	GT	GG	U58033	MTMR2: myotubularin related protein 2
900123	ADR	AA	AG	null	U58033	MTMR2: myotubularin related protein 2
900124	EFF	GG	AG	AA	U58033	MTMR2: myotubularin related protein 2
900132	ADR	TT	CT	CC	AF169257	SLC24A3: solute carrier family 24 (sodium/potassium/calcium exchanger), member 3
900144	CVD	AA	AG	GG	AC008945	Selenoprotein P genomic region
900144	ADR5	AA	AG	GG	AC008945	Selenoprotein P genomic region
900145	CVD	GG	GT	TT	AC008945	Selenoprotein P genomic region

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
900145	ADR5	GG	GT	TT	AC008945	Selenoprotein P genomic region
900146	ADR5	AA	AG	GG	AC008945	Selenoprotein P genomic region
900146	CVD	AA	AG	GG	AC008945	Selenoprotein P genomic region
900146	ADR	AA	AG	GG	AC008945	Selenoprotein P genomic region
900147	ADR3	TT	CT	CC	AC008945	Selenoprotein P genomic region
900196	CVD	CC	CT	TT	G62788	SHGC-140326 Human Homo sapiens STS genomic, sequence tagged site.
900196	ADR3	CC	CT	TT	G62788	SHGC-140326 Human Homo sapiens STS genomic, sequence tagged site.
900200	CVD	TT	CT	CC	AF101918	Human Homo sapiens genomic clone pTWB28.01, DNA sequence.
900204	EFF	CC	CG	null	NM_016347	N-Acetyltransferase Camello 2
900205	EFF	CC	CG	GG	NM_016347	N-Acetyltransferase Camello 2
900205	CVD	CC	CG	GG	NM_016347	N-Acetyltransferase Camello 2
900223	ADR	GG	AG	AA	AK055126	HS cDNA FLJ30564 fis
900225	ADR5	GG	AG	AA	AJ227891	Homo sapiens partial mRNA; ID ED166-4A2
900225	ADR3	GG	AG	AA	AJ227891	Homo sapiens partial mRNA; ID ED166-4A2
900227	ADR5	AA	AC	CC	SECONDARY: AJ000414	SECONDARY TO Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)
900233	ADR5	TT	AT	AA	SECONDARY: AJ000414	SECONDARY TO Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)
900236	ADR3	CC	CT	TT	SECONDARY: AJ000414	SECONDARY TO Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)
900236	ADR5	CC	CT	TT	SECONDARY: AJ000414	SECONDARY TO Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)
900241	EFF	CC	CG	GG	SECONDARY:	SECONDARY TO Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)

BAYSNP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
					AJ000414	
900242	ADR5	GG	CG	CC	SECONDARY: AJ000414	SECONDARY TO Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)
900242	ADR3	GG	CG	CC	SECONDARY: AJ000414	SECONDARY TO Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)
900242	ADR	GG	CG	CC	SECONDARY: AJ000414	SECONDARY TO Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)

Table 4 **Cohorts**

Given are names (as used in table 5) and formations of the various cohorts that were used for genotyping

COHORT	Definition
HELD_ALL_GOOD/BAD	Healthy elderly individuals of both genders with good or bad serum lipid profiles (as defined in table 1a)
HELD_FEM_GOOD/BAD	Healthy elderly individuals (female) with good or bad serum lipid profiles (as defined in table 1a)
HELD_MAL_GOOD/BAD	Healthy elderly individuals (male) with good or bad serum lipid profiles (as defined in table 1a)
CVD_ALL_CASE/CTRL	Individuals with diagnosis of cardiovascular disease and healthy controls (both genders)
CVD_FEM_CASE/CTRL	Individuals with diagnosis of cardiovascular disease and healthy controls (female)
CVD_MAL_CASE/CTRL	Individuals with diagnosis of cardiovascular disease and healthy controls (male)
HELD_FEM_ADRCTRL	Female individuals that tolerate adminstration of cerivastatin without exhibiting signs of ADR (as defined in table 1b)
HELD_FEM_ADRCASE	Female individuals that exhibited ADR (as defined in table 1b) upon administration of cerivastatin
HELD_MAL_ADRCTRL	Male individuals that tolerate adminstration of cerivastatin without exhibiting signs of ADR (as defined in table 1b)
HELD_MAL_ADRCASE	Male individuals that exhibited ADR (as defined in table 1b) upon administration of cerivastatin
HELD_ALL_ADRCTRL	Individuals of both genders that tolerate adminstration of cerivastatin without exhibiting signs of ADR (as defined in table 1b)
HELD_ALL_ADRCASE	Individuals of both genders that exhibited ADR (as defined in table 1b) upon administration of cerivastatin
HELD_FEM_LORESP	Female individuals with a minor response to cerivastatin administration (as defined in table 1b)
HELD_FEM_HIRESP	Female individuals with a high response to to cerivastatin administration (as defined in table 1b)
HELD_FEM_HIHDL/LOHDL	Healthy elderly individuals (female) with high or low serum HDL cholesterol levels (as defined in table 1c)
HELD_MAL_HIHDL/LOHDL	Healthy elderly individuals (male) with high or low serum HDL cholesterol levels (as defined in table 1c)
HELD_ALL_HIHDL/LOHDL	Healthy elderly individuals of both genders with high or low serum HDL cholesterol levels (as defined in table 1c)
HELD_FEM_ADR3CASE	Female individuals that exhibited advanced ADR (as defined in table 1b) upon administration of cerivastatin

COHORT	Definition
HELD_MAL_ADR3CASE	Male individuals that exhibited advanced ADR (as defined in table 1b) upon administration of cerivastatin
HELD_ALL_ADR3CASE	Individuals of both genders that exhibited advanced ADR (as defined in table 1b) upon administration of cerivastatin
HELD_FEM_VLORESP	Female individuals with a very low response to cerivastatin administration (as defined in table 1b)
HELD_FEM_VHIRESP	Female individuals with a very high response to cerivastatin administration (as defined in table 1b)
HELD_FEM_ADR5CASE	Female individuals that exhibited severe ADR (as defined in table 1b) upon administration of cerivastatin
HELD_MAL_ADR5CASE	Male individuals that exhibited severe ADR (as defined in table 1b) upon administration of cerivastatin
HELD_ALL_ADR5CASE	Individuals of both genders that exhibited severe ADR (as defined in table 1b) upon administration of cerivastatin
HELD_FEM_ULORESP	Female individuals with a ultra low response to cerivastatin administration (as defined in table 1b)
HELD_FEM_UHIRESP	Female individuals with a ultra high response to to cerivastatin administration (as defined in table 1b)

Table 5a and 5b **Cohort sizes and p-values of PA SNPs**

The baySNP number refers to an internal numbering of the PA SNPs. Cpval denotes the classical Pearson chi-squared test, Xpval denotes the exact version of Pearson's chi-squared test, LRpval denotes the likelihood-ratio chi-squared test,. Cpvalue, Xpvalue, and LRpvalue are calculated as described in (SAS/STAT User's Guide of the SAS OnlineDoc, Version 8), (L. D. Fisher and G. van Belle, Biostatistics, Wiley Interscience 1993), and (A. Agresti, Statistical Science 7, 131 (1992)).The GTYPE and Allele p values were obtained through the respective chi square tests when comparing COHORTs A and B. For GTYPE p value the number of patients in cohort A carrying genotypes 11, 12 or 22 (FQ11 A, FQ 12 A, FQ 22 A; genotypes as defined in table 3) were compared with the respective patients in cohort B (FQ11 B, FQ 12 B, FQ 22 B; genotypes as defined in table 3) resulting in the respective chi square test with a 3×2 matrix. For Allele p values we compared the allele count of alleles 1 and 2 (A1 and A2) in cohorts A and B, respectively (chi square test with a 2×2 matrix). SIZE A and B: Number of patients in cohorts A and B, respectively. See table 4 for definition of COHORTs A and B.

Table 5a Cohort sizes and frequency of alleles and genotypes

baySNP	A1	A2	COHORT_A	SIZE A	FQ1 A	FQ2 A	FQ11 A	FQ12 A	FQ22 A	COHORT_B	SIZE B	FQ1 B	FQ2 B	FQ11 B	FQ12 B	FQ22 B
29	A	G	HELD_FEM_BAD	80	100	60	32	36	12	HELD_FEM_GOOD	78	80	76	19	42	17
29	A	G	HELD_ALL_ADRCASE3ULN	47	54	40	21	12	14	HELD_ALL_ADRCTRL	131	125	137	35	55	41
29	A	G	HELD_ALL_BAD	99	122	76	39	44	16	HELD_ALL_GOOD	114	119	109	29	61	24
52	C	G	HELD_ALL_CASE	43	42	44	11	20	12	HELD_ALL_CTRL	39	57	21	22	13	4
52	C	G	HELD_MAL_LOHDL	18	20	16	3	14	1	HELD_MAL_HIHDL	25	29	21	10	9	6
52	C	G	HELD_FEM_CASE	29	27	31	6	15	8	HELD_FEM_CTRL	22	30	14	11	8	3

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1_A	FQ2_A	FQ11_A	FQ12_A	FQ22_A	COHORT_B	SIZE_B	FQ1_B	FQ2_B	FQ11_B	FQ12_B	FQ22_B
52	C	G	HELD_MAL_CASE	14	15	13	5	5	4	HELD_MAL_CTRL	17	27	7	11	5	1
52	C	G	HELD_MAL_BAD2	253	254	252	60	134	59	HELD_MAL_GOOD2	281	317	245	87	143	51
57	C	T	HELD_FEM_CASE	31	45	17	15	15	1	HELD_FEM_CTRL	22	41	3	19	3	0
118	C	T	HELD_MAL_BAD2	306	493	119	196	101	9	HELD_MAL_GOOD2	337	512	162	194	124	19
137	G	A	HELD_MAL_ADRCASE5ULN	8	7	9	0	7	1	HELD_MAL_ADRCTRL	54	71	37	23	25	6
137	G	A	HELD_ALL_ADRCASE5ULN	23	25	21	3	19	1	HELD_ALL_ADRCTRL	119	151	87	44	63	12
137	G	A	HELD_ALL_ADRCASE3ULN	44	46	42	7	32	5	HELD_ALL_ADRCTRL	119	151	87	44	63	12
179	G	A	HELD_MAL_ADRCASE5ULN	8	14	2	7	0	1	HELD_MAL_ADRCTRL	56	97	15	41	15	0
179	G	A	HELD_MAL_ADRCASE3ULN	16	29	3	14	1	1	HELD_MAL_ADRCTRL	56	97	15	41	15	0
179	G	A	HELD_ALL_ADRCASE5ULN	25	45	5	21	3	1	HELD_ALL_ADRCTRL	124	219	29	95	29	0
179	G	A	HELD_ALL_ADRCASE	128	234	22	108	18	2	HELD_ALL_ADRCTRL	124	219	29	95	29	0
240	G	C	HELD_ALL_ADRCASE3ULN	44	83	5	39	5	0	HELD_ALL_ADRCTRL	130	224	36	96	32	2
240	G	C	HELD_MAL_ADRCASE3ULN	17	33	1	16	1	0	HELD_MAL_ADRCTRL	59	102	16	43	16	0
241	G	A	HELD_ALL_ADRCASE3ULN	47	60	34	20	20	7	HELD_ALL_ADRCTRL	129	196	62	77	42	10
241	G	A	HELD_ALL_ADRCASE5ULN	25	31	19	10	11	4	HELD_ALL_ADRCTRL	129	196	62	77	42	10
241	G	A	HELD_MAL_ADRCASE3ULN	17	19	15	6	7	4	HELD_MAL_ADRCTRL	58	86	30	35	16	7
288	G	C	CVD_ALL_CASE	101	146	56	51	44	6	CVD_ALL_CTRL	73	119	27	47	25	1
384	C	G	CVD_ALL_CASE	104	123	85	43	37	24	CVD_ALL_CTRL	74	77	71	18	41	15
384	C	G	HELD_FEM_CASE	31	38	24	12	14	5	HELD_FEM_CTRL	22	17	27	3	11	8
533	G	A	CVD_ALL_CASE	103	162	44	62	38	3	CVD_ALL_CTRL	74	129	19	56	17	1
542	G	A	HELD_FEM_ADRCASE	73	118	28	45	28	0	HELD_FEM_ADRCTRL	71	125	17	55	15	1

baySNP	A1	A2	COHORT_A	SIZE A	FQ1 A	FQ2 A	FQ11 A	FQ12 A	FQ22 A	COHORT_B	SIZE B	FQ1 B	FQ2 B	FQ11 B	FQ12 B	FQ22 B
576	C	T	HELD_ALL_BAD	100	200	0	100	0	0	HELD_ALL_GOOD	115	225	5	110	5	0
576	C	T	HELD_FEM_BAD	81	162	0	81	0	0	HELD_FEM_GOOD	79	154	4	75	4	0
608	G	A	CVD_MAL_CASE	68	120	16	52	16	0	CVD_MAL_CTRL	33	47	19	19	9	5
614	G	A	HELD_MAL_LOHDL	20	30	10	15	0	5	HELD_MAL_HIHDL	26	0	52	26	0	0
614	G	A	HELD_ALL_CASE	44	57	31	21	15	8	HELD_ALL_CTRL	40	67	13	32	3	5
614	G	A	HELD_MAL_CASE	13	12	14	6	0	7	HELD_MAL_CTRL	18	28	8	14	0	4
614	G	A	HELD_MAL_BAD	19	21	17	10	1	8	HELD_MAL_GOOD	35	55	15	27	1	7
614	G	A	CVD_ALL_CASE	96	126	66	53	20	23	CVD_ALL_CTRL	63	98	28	44	10	9
614	G	A	HELD_FEM_CASE	31	45	17	15	15	1	HELD_FEM_CTRL	22	39	5	18	3	1
738	A	C	CVD_ALL_CASE	104	106	102	29	48	27	CVD_ALL_CTRL	74	93	55	30	33	11
1056	A	G	HELD_ALL_LOHDL	34	51	17	21	9	4	HELD_ALL_HIHDL	50	59	41	19	21	10
1056	A	G	HELD_FEM_BAD	78	98	58	32	34	12	HELD_FEM_GOOD	78	113	43	38	37	3
1092	G	C	HELD_MAL_ADRCASE5ULN	8	12	4	6	0	2	HELD_MAL_ADRCTRL	59	82	36	28	26	5
1524	C	A	HELD_MAL_CASE2	44	56	32	16	24	4	HELD_MAL_CTRL2	26	44	8	19	6	1
1524	C	A	HELD_ALL_BAD	96	151	41	55	41	0	HELD_ALL_GOOD	112	158	66	50	58	4
1524	C	A	HELD_ALL_CASE	44	72	16	29	14	1	HELD_ALL_CTRL	39	52	26	19	14	6
1574	T	C	CVD_MAL_CASE	69	119	19	53	13	3	CVD_MAL_CTRL	34	55	13	21	13	0
1582	T	C	HELD_MAL_ADRCASE3ULN	16	30	2	14	2	0	HELD_MAL_ADRCTRL	53	83	23	33	17	3
1657	C	T	HELD_FEM_HIRESP	23	29	17	11	7	5	HELD_FEM_LORESP	33	37	29	8	21	4
1722	T	C	CVD_MAL_CASE	63	79	47	31	17	15	CVD_MAL_CTRL	33	37	29	9	19	5
1756	C	T	HELD_MAL_ADRCASE5ULN	9	14	4	6	2	1	HELD_MAL_ADRCTRL	56	104	8	48	8	0

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1 A	FQ2 A	FQ11 A	FQ12 A	FQ22 A	COHORT_B	SIZE_B	FQ1 B	FQ2 B	FQ11 B	FQ12 B	FQ22 B
1757	G	A	HELD_ALL_CASE	45	63	27	25	13	7	HELD_ALL_CTRL	38	58	18	20	18	0
1757	G	A	HELD_FEM_CASE	31	40	22	16	8	7	HELD_FEM_CTRL	21	33	9	12	9	0
1757	G	A	HELD_FEM_VHIRESP	148	177	119	52	73	23	HELD_FEM_VLORESP	152	206	98	70	66	16
1757	G	A	HELD_MAL_ADRCASE	62	90	34	30	30	2	HELD_MAL_ADRCTRL	58	87	29	35	17	6
1765	A	G	HELD_ALL_BAD	100	29	171	6	17	77	HELD_ALL_GOOD	107	39	175	3	33	71
1767	T	C	HELD_ALL_ADRCASE3ULN	40	75	5	36	3	1	HELD_ALL_ADRCTRL	107	172	42	69	34	4
1767	T	C	HELD_ALL_ADRCASE5ULN	21	40	2	19	2	0	HELD_ALL_ADRCTRL	107	172	42	69	34	4
1767	T	C	HELD_MAL_ADRCASE5ULN	7	0	14	7	0	0	HELD_MAL_ADRCTRL	53	86	20	35	16	2
1767	T	C	HELD_FEM_ADRCASE3ULN	27	50	4	24	2	1	HELD_FEM_ADRCTRL	54	86	22	34	18	2
1767	T	C	HELD_MAL_ADRCASE3ULN	13	25	1	12	1	0	HELD_MAL_ADRCTRL	53	86	20	35	16	2
1837	C	T	HELD_ALL_ADRCASE3ULN	48	75	21	29	17	2	HELD_ALL_ADRCTRL	132	173	91	52	69	11
1837	C	T	HELD_FEM_BAD	81	120	42	49	22	10	HELD_FEM_GOOD	79	109	49	36	37	6
1837	C	T	HELD_ALL_BAD	100	145	55	58	29	13	HELD_ALL_GOOD	115	158	72	53	52	10
1837	C	T	HELD_ALL_ADRCASE	134	195	73	72	51	11	HELD_ALL_ADRCTRL	132	173	91	52	69	11
1854	A	G	HELD_FEM_BAD	80	85	75	21	43	16	HELD_FEM_GOOD	79	100	58	35	30	14
1862	C	T	HELD_FEM_BAD	80	121	39	44	33	3	HELD_FEM_GOOD	76	97	55	29	39	8
2085	G	T	HELD_FEM_CASE	31	44	18	14	16	1	HELD_FEM_CTRL	22	20	24	4	12	6
2085	G	T	HELD_ALL_CASE	45	61	29	19	23	3	HELD_ALL_CTRL	40	40	40	10	20	10
2093	C	T	HELD_MAL_CASE	14	15	13	7	1	6	HELD_MAL_CTRL	18	32	4	16	0	2
2093	C	T	HELD_ALL_CASE	45	62	28	25	12	8	HELD_ALL_CTRL	40	66	14	28	10	2
2109	A	G	HELD_MAL_LOHDL	19	34	4	16	2	1	HELD_MAL_HIHDL	22	31	13	9	13	0

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1 A	FQ2 A	FQ11 A	FQ12 A	FQ22 A	COHORT_B	SIZE_B	FQ1 B	FQ2 B	FQ11 B	FQ12 B	FQ22 B
2109	A	G	HELD_ALL_LOHDL	39	70	8	32	6	1	HELD_ALL_HIHDL	48	76	20	28	20	0
2109	A	G	HELD_ALL_BAD2	624	1035	213	432	171	21	HELD_ALL_GOOD2	700	1109	291	439	231	30
2109	A	G	HELD_FEM_BAD	80	139	21	60	19	1	HELD_FEM_GOOD	78	120	36	45	30	3
2124	G	T	HELD_MAL_BAD	17	14	20	7	0	10	HELD_MAL_GOOD	32	40	24	20	0	12
2140	G	T	HELD_FEM_UHIRESP	43	79	7	36	7	0	HELD_FEM_ULORESP	60	94	26	38	18	4
2140	G	T	HELD_FEM_HIRESP	237	416	58	181	54	2	HELD_FEM_LORESP	239	390	88	161	68	10
2140	G	T	HELD_MAL_ADRCASE	46	80	12	34	12	0	HELD_MAL_ADRCTRL	49	73	25	29	15	5
2140	G	T	HELD_FEM_VHIRESP	119	207	31	90	27	2	HELD_FEM_VLORESP	122	194	50	77	40	5
2141	G	A	HELD_MAL_ADRCASE3ULN	16	30	2	14	2	0	HELD_MAL_ADRCTRL	52	78	26	30	18	4
2141	G	A	HELD_FEM_UHIRESP	53	91	15	38	15	0	HELD_FEM_ULORESP	77	121	33	51	19	7
2141	G	A	HELD_MAL_ADRCASE	58	100	16	42	16	0	HELD_MAL_ADRCTRL	52	78	26	30	18	4
2186	T	C	HELD_MAL_ADRCASE5ULN	9	14	4	6	2	1	HELD_MAL_ADRCTRL	59	109	9	50	9	0
2187	C	T	HELD_FEM_ADRCASE3ULN	30	37	23	10	17	3	HELD_FEM_ADRCTRL	71	107	35	42	23	6
2192	G	A	HELD_FEM_ADRCASE	69	137	1	68	1	0	HELD_FEM_ADRCTRL	70	127	13	57	13	0
2192	G	A	HELD_FEM_ADRCASE3ULN	30	0	60	30	0	0	HELD_FEM_ADRCTRL	70	127	13	57	13	0
2192	G	A	HELD_ALL_ADRCASE	132	258	6	126	6	0	HELD_ALL_ADRCTRL	126	233	19	108	17	1
2192	G	A	HELD_FEM_ADRCASE5ULN	16	0	32	16	0	0	HELD_FEM_ADRCTRL	70	127	13	57	13	0
2192	G	A	HELD_ALL_ADRCASE3ULN	47	92	2	45	2	0	HELD_ALL_ADRCTRL	126	233	19	108	17	1
2203	T	C	HELD_FEM_BAD	80	106	54	32	42	6	HELD_FEM_GOOD	79	125	33	50	25	4
2203	T	C	HELD_ALL_BAD	98	128	68	39	50	9	HELD_ALL_GOOD	115	171	59	66	39	10
2217	G	T	HELD_MAL_CASE	13	14	12	2	10	1	HELD_MAL_CTRL	17	29	5	12	5	0

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1 A	FQ2 A	FQ11 A	FQ12 A	FQ22 A	COHORT_B	SIZE_B	FQ1 B	FQ2 B	FQ11 B	FQ12 B	FQ22 B
2217	G	T	CVD_FEM_CASE	33	63	3	30	3	0	CVD_FEM_CTRL	40	68	12	30	8	2
2281	A	C	HELD_FEM_CASE	31	26	36	6	14	11	HELD_FEM_CTRL	22	30	14	11	8	3
2281	A	C	HELD_MAL_CASE	14	20	8	6	8	0	HELD_MAL_CTRL	18	18	18	6	6	6
2284	G	A	HELD_MAL_BAD	17	32	2	15	2	0	HELD_MAL_GOOD	35	53	17	20	13	2
2290	A	G	HELD_MAL_CASE	14	18	10	9	0	5	HELD_MAL_CTRL	18	34	2	17	0	1
2327	A	C	HELD_MAL_ADRCASE	59	70	48	26	18	15	HELD_MAL_ADRCTRL	54	52	56	12	28	14
2327	A	C	HELD_MAL_ADRCASE5ULN	9	11	7	5	1	3	HELD_MAL_ADRCTRL	54	52	56	12	28	14
2327	A	C	HELD_MAL_ADRCASE3ULN	17	22	12	9	4	4	HELD_MAL_ADRCTRL	54	52	56	12	28	14
2327	A	C	HELD_FEM_HIRESP	270	249	291	63	123	84	HELD_FEM_LORESP	281	287	275	68	151	62
2353	A	G	CVD_MAL_CASE	66	117	15	52	13	1	CVD_MAL_CTRL	21	42	0	21	0	0
2353	A	G	HELD_ALL_CASE	45	83	7	40	3	2	HELD_ALL_CTRL	38	63	13	26	11	1
2353	A	G	CVD_ALL_CASE	100	178	22	79	20	1	CVD_ALL_CTRL	49	94	4	45	4	0
2353	A	G	HELD_FEM_CASE	31	58	4	28	2	1	HELD_FEM_CTRL	21	36	6	15	6	0
2371	A	C	HELD_ALL_BAD2	630	927	333	332	263	35	HELD_ALL_GOOD2	726	1117	335	434	249	43
2376	C	T	HELD_ALL_BAD2	620	1193	47	573	47	0	HELD_ALL_GOOD2	717	1400	34	683	34	0
2401	T	G	HELD_FEM_UHIRESP	52	76	28	26	24	2	HELD_FEM_ULORESP	73	119	27	51	17	5
2463	T	C	HELD_ALL_CASE	44	81	7	37	7	0	HELD_ALL_CTRL	36	0	72	36	0	0
2463	T	C	HELD_FEM_CASE	30	54	6	24	6	0	HELD_FEM_CTRL	22	0	44	22	0	0
2463	T	C	HELD_FEM_BAD2	307	572	42	265	42	0	HELD_FEM_GOOD2	370	693	47	327	39	4
2755	A	G	HELD_FEM_ADRCASE	72	69	75	19	31	22	HELD_FEM_ADRCTRL	70	86	54	24	38	8
2755	A	G	HELD_ALL_ADRCASE	134	147	121	44	59	31	HELD_ALL_ADRCTRL	128	162	94	48	66	14

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1_A	FQ2_A	FQ11_A	FQ12_A	FQ22_A	COHORT_B	SIZE_B	FQ1_B	FQ2_B	FQ11_B	FQ12_B	FQ22_B
2755	A	G	HELD_FEM_HIRESP	271	331	211	96	139	36	HELD_FEM_LORESP	284	333	235	106	121	57
2925	G	A	HELD_FEM_VHIRESP	141	163	119	48	67	26	HELD_FEM_VLORESP	145	134	156	29	76	40
2925	G	A	HELD_FEM_UHIRESP	54	64	44	18	28	8	HELD_FEM_ULORESP	77	66	88	11	44	22
3043	G	A	HELD_FEM_ADRCASE3ULN	17	32	2	15	2	0	HELD_FEM_ADRCTRL	31	49	13	18	13	0
3152	T	A	HELD_FEM_VHIRESP	107	125	89	42	41	24	HELD_FEM_VLORESP	108	116	100	46	24	38
3214	C	G	HELD_FEM_VHIRESP	151	253	49	103	47	1	HELD_FEM_VLORESP	142	231	53	97	37	8
3215	C	G	HELD_MAL_ADRCASE5ULN	9	17	1	8	1	0	HELD_MAL_ADRCTRL	60	120	0	60	0	0
3237	C	G	HELD_FEM_CASE	28	55	1	27	1	0	HELD_FEM_CTRL	18	31	5	13	5	0
3241	T	C	HELD_MAL_ADRCASE	45	57	33	18	21	6	HELD_MAL_ADRCTRL	51	49	53	13	23	15
3826	C	A	HELD_MAL_ADRCASE5ULN	7	0	14	7	0	0	HELD_MAL_ADRCTRL	44	71	17	30	11	3
3826	C	A	HELD_ALL_ADRCASE5ULN	18	35	1	17	1	0	HELD_ALL_ADRCTRL	90	156	24	70	16	4
3826	C	A	HELD_MAL_ADRCASE3ULN	12	23	1	11	1	0	HELD_MAL_ADRCTRL	44	71	17	30	11	3
3842	C	G	CVD_ALL_CASE	100	190	10	90	10	0	CVD_ALL_CTRL	63	126	0	63	0	0
3842	C	G	CVD_MAL_CASE	68	129	7	61	7	0	CVD_MAL_CTRL	30	60	0	30	0	0
3842	C	G	CVD_FEM_CASE	32	61	3	29	3	0	CVD_FEM_CTRL	33	66	0	33	0	0
3843	A	T	HELD_MAL_CASE2	23	32	14	9	14	0	HELD_MAL_CTRL2	17	17	17	5	7	5
3843	A	T	HELD_FEM_LOHDL	12	11	13	0	11	1	HELD_FEM_HIHDL	15	20	10	6	8	1
3869	G	T	HELD_FEM_UHIRESP	53	76	30	29	18	6	HELD_FEM_ULORESP	73	84	62	24	36	13
3942	C	A	HELD_FEM_UHIRESP	54	91	17	40	11	3	HELD_FEM_ULORESP	74	141	7	67	7	0
4018	T	C	HELD_MAL_BAD	18	30	6	12	6	0	HELD_MAL_GOOD	36	46	26	15	16	5
4206	A	T	HELD_ALL_ADRCASE3ULN	48	47	49	11	25	12	HELD_ALL_ADRCTRL	132	161	103	47	67	18

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1_A	FQ2_A	FQ11_A	FQ12_A	FQ22_A	COHORT_B	SIZE_B	FQ1_B	FQ2_B	FQ11_B	FQ12_B	FQ22_B
4206	A	T	HELD_FEM_ADRCASE	72	72	72	17	38	17	HELD_FEM_ADRCTRL	72	89	55	27	35	10
4206	A	T	HELD_ALL_ADRCASE5ULN	26	24	28	5	14	7	HELD_ALL_ADRCTRL	132	161	103	47	67	18
4527	G	A	CVD_ALL_CASE	71	114	28	43	28	0	CVD_ALL_CTRL	54	80	28	33	14	7
4527	G	A	HELD_FEM_BAD2	320	508	132	199	110	11	HELD_FEM_GOOD2	370	546	194	199	148	23
4527	G	A	HELD_MAL_CASE	12	17	7	6	5	1	HELD_MAL_CTRL	16	30	2	14	2	0
4527	G	A	HELD_MAL_CASE2	45	71	19	27	17	1	HELD_MAL_CTRL2	29	36	22	11	14	4
4527	G	A	HELD_ALL_ADRCASE3ULN	48	68	28	22	24	2	HELD_ALL_ADRCTRL	124	202	46	80	42	2
4527	G	A	HELD_ALL_CASE2	104	162	46	63	36	5	HELD_ALL_CTRL2	71	97	45	34	29	8
4527	G	A	HELD_ALL_ADRCASE5ULN	26	36	16	12	12	2	HELD_ALL_ADRCTRL	124	202	46	80	42	2
4544	G	A	HELD_MAL_ADRCASE3ULN	17	20	14	5	10	2	HELD_MAL_ADRCTRL	59	97	21	39	19	1
4544	G	A	HELD_MAL_ADRCASE	62	87	37	31	25	6	HELD_MAL_ADRCTRL	59	97	21	39	19	1
4544	G	A	HELD_ALL_ADRCASE	133	183	83	63	57	13	HELD_ALL_ADRCTRL	130	201	59	77	47	6
4544	G	A	HELD_ALL_ADRCASE3ULN	47	63	31	20	23	4	HELD_ALL_ADRCTRL	130	201	59	77	47	6
4545	G	A	HELD_MAL_ADRCASE3ULN	17	20	14	5	10	2	HELD_MAL_ADRCTRL	59	97	21	39	19	1
4545	G	A	HELD_MAL_ADRCASE	61	85	37	30	25	6	HELD_MAL_ADRCTRL	59	97	21	39	19	1
4545	G	A	HELD_ALL_ADRCASE	132	181	83	62	57	13	HELD_ALL_ADRCTRL	128	197	59	75	47	6
4668	C	A	HELD_ALL_ADRCASE5ULN	26	34	18	9	16	1	HELD_ALL_ADRCTRL	130	139	121	39	61	30
4669	C	T	HELD_FEM_HIRESP	286	474	98	195	84	7	HELD_FEM_LORESP	281	490	72	214	62	5
4718	G	A	HELD_MAL_BAD	18	26	10	8	10	0	HELD_MAL_GOOD	34	41	27	16	9	9
4818	G	A	HELD_MAL_BAD	17	20	14	3	14	0	HELD_MAL_GOOD	36	54	18	20	14	2
4827	A	G	HELD_MAL_ADRCASE5ULN	9	15	3	7	1	1	HELD_MAL_ADRCTRL	59	103	15	44	15	0

baySNP	A1	A2	COHORT_A	SIZE A	FQ1 A	FQ2 A	FQ11 A	FQ12 A	FQ22 A	COHORT_B	SIZE_B	FQ1 B	FQ2 B	FQ11 B	FQ12 B	FQ22 B
4838	A	G	HELD_ALL_CASE2	101	113	89	32	49	20	HELD_ALL_CTRL2	71	64	78	16	32	23
4856	G	A	CVD_MAL_CASE	69	0	138	69	0	0	CVD_MAL_CTRL	34	65	3	31	3	0
4868	T	C	HELD_MAL_ADRCASE	62	88	36	32	24	6	HELD_MAL_ADRCTRL	59	92	26	33	26	0
4868	T	C	HELD_MAL_ADRCASE5ULN	8	11	5	4	3	1	HELD_MAL_ADRCTRL	59	92	26	33	26	0
4887	C	A	HELD_MAL_CASE	14	26	2	12	2	0	HELD_MAL_CTRL	18	23	13	6	11	1
4887	C	A	HELD_ALL_CASE	45	75	15	31	13	1	HELD_ALL_CTRL	38	53	23	17	19	2
4912	G	A	HELD_MAL_BAD	12	7	17	3	1	8	HELD_MAL_GOOD	31	34	28	15	4	12
4951	G	A	HELD_ALL_ADRCASE3ULN	48	51	45	19	13	16	HELD_ALL_ADRCTRL	128	145	111	37	71	20
4951	G	A	HELD_FEM_ADRCASE3ULN	31	29	33	10	9	12	HELD_FEM_ADRCTRL	69	77	61	17	43	9
4951	G	A	HELD_FEM_ADRCASE5ULN	17	13	21	4	5	8	HELD_FEM_ADRCTRL	69	77	61	17	43	9
4951	G	A	HELD_ALL_ADRCASE5ULN	26	22	30	7	8	11	HELD_ALL_ADRCTRL	128	145	111	37	71	20
4951	G	A	HELD_FEM_ADRCASE	73	68	78	19	30	24	HELD_FEM_ADRCTRL	69	77	61	17	43	9
4951	G	A	HELD_ALL_ADRCASE	135	135	135	39	57	39	HELD_ALL_ADRCTRL	128	145	111	37	71	20
4952	T	C	HELD_ALL_ADRCASE3ULN	48	52	44	20	12	16	HELD_ALL_ADRCTRL	128	145	111	38	69	21
4952	T	C	HELD_FEM_ADRCASE3ULN	31	30	32	11	8	12	HELD_FEM_ADRCTRL	70	80	60	19	42	9
4952	T	C	HELD_FEM_ADRCASE5ULN	17	14	20	5	4	8	HELD_FEM_ADRCTRL	70	80	60	19	42	9
4952	T	C	HELD_ALL_ADRCASE5ULN	26	23	29	8	7	11	HELD_ALL_ADRCTRL	128	145	111	38	69	21
4966	G	A	HELD_MAL_BAD	18	27	9	9	9	0	HELD_MAL_GOOD	34	34	34	7	20	7
4966	G	A	HELD_MAL_ADRCASE	61	68	54	20	28	13	HELD_MAL_ADRCTRL	59	53	65	8	37	14
4966	G	A	HELD_FEM_CASE	30	25	35	4	17	9	HELD_FEM_CTRL	21	26	16	8	10	3
5019	A	T	CVD_FEM_CASE	32	25	39	3	19	10	CVD_FEM_CTRL	34	43	25	17	9	8

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1 A	FQ2 A	FQ11 A	FQ12 A	FQ22 A	COHORT_B	SIZE_B	FQ1 B	FQ2 B	FQ11 B	FQ12 B	FQ22 B
5019	A	T	HELD_ALL_CASE2	87	96	78	23	50	14	HELD_ALL_CTRL2	62	54	70	16	22	24
5019	A	T	HELD_MAL_LOHDL	18	27	9	11	5	2	HELD_MAL_HIHDL	22	20	24	6	8	8
5019	A	T	HELD_ALL_BAD	86	95	77	29	37	20	HELD_ALL_GOOD	100	84	116	25	34	41
5019	A	T	HELD_MAL_CASE2	37	43	31	12	19	6	HELD_MAL_CTRL2	24	17	31	5	7	12
5165	C	A	HELD_FEM_ADRCASE3ULN	30	46	14	16	14	0	HELD_FEM_ADRCTRL	70	122	18	54	14	2
5165	C	A	HELD_MAL_ADRCASE5ULN	9	15	3	7	1	1	HELD_MAL_ADRCTRL	59	103	15	44	15	0
5165	C	A	HELD_FEM_ADRCASE	71	116	26	45	26	0	HELD_FEM_ADRCTRL	70	122	18	54	14	2
5165	C	A	HELD_FEM_ADRCASE5ULN	16	24	8	8	8	0	HELD_FEM_ADRCTRL	70	122	18	54	14	2
5278	G	A	HELD_MAL_ADRCASE5ULN	9	10	8	3	4	2	HELD_MAL_ADRCTRL	60	93	27	35	23	2
5287	C	T	HELD_FEM_VHIRESP	159	257	61	108	41	10	HELD_FEM_VLORESP	147	260	34	116	28	3
5320	A	G	CVD_FEM_CASE	33	40	26	11	18	4	CVD_FEM_CTRL	38	32	44	9	14	15
5324	T	C	HELD_FEM_VHIRESP	137	124	150	31	62	44	HELD_FEM_VLORESP	134	146	122	40	66	28
5373	G	T	HELD_FEM_ADRCASE5ULN	16	29	3	13	3	0	HELD_FEM_ADRCTRL	71	94	48	28	38	5
5373	G	T	HELD_ALL_ADRCASE5ULN	25	42	8	17	8	0	HELD_ALL_ADRCTRL	131	180	82	60	60	11
5375	C	T	HELD_FEM_ADRCASE5ULN	15	27	3	12	3	0	HELD_FEM_ADRCTRL	70	90	50	26	38	6
5375	C	T	HELD_ALL_ADRCASE5ULN	24	39	9	15	9	0	HELD_ALL_ADRCTRL	128	173	83	57	59	12
5376	A	T	HELD_MAL_ADRCASE5ULN	8	15	1	7	1	0	HELD_MAL_ADRCTRL	58	116	0	58	0	0
5377	T	C	HELD_FEM_ADRCASE	60	88	32	35	18	7	HELD_FEM_ADRCTRL	64	85	43	25	35	4
5377	T	C	HELD_FEM_ADRCASE5ULN	15	26	4	11	4	0	HELD_FEM_ADRCTRL	64	85	43	25	35	4
5517	A	G	HELD_MAL_ADRCASE	53	104	2	52	0	1	HELD_MAL_ADRCTRL	55	106	4	51	4	0
5518	G	C	HELD_FEM_ADRCASE5ULN	16	31	1	15	1	0	HELD_FEM_ADRCTRL	71	0	142	71	0	0

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1 A	FQ2 A	FQ11 A	FQ12 A	FQ22 A	COHORT_B	SIZE_B	FQ1 B	FQ2 B	FQ11 B	FQ12 B	FQ22 B
5564	G	T	CVD_MAL_CASE	69	73	65	11	51	7	CVD_MAL_CTRL	34	44	24	14	16	4
5569	G	A	HELD_MAL_ADRCASE5ULN	8	15	1	7	1	0	HELD_MAL_ADRCTRL	53	74	32	25	24	4
5569	G	A	HELD_ALL_ADRCASE5ULN	22	37	7	15	7	0	HELD_ALL_ADRCTRL	122	170	74	60	50	12
5716	G	C	HELD_ALL_ADRCASE3ULN	44	34	54	6	22	16	HELD_ALL_ADRCTRL	109	126	92	34	58	17
5716	G	C	HELD_FEM_ADRCASE3ULN	29	18	40	2	14	13	HELD_FEM_ADRCTRL	59	65	53	16	33	10
5716	G	C	HELD_ALL_ADRCASE5ULN	22	16	28	2	12	8	HELD_ALL_ADRCTRL	109	126	92	34	58	17
5716	G	C	HELD_FEM_ADRCASE5ULN	15	10	20	1	8	6	HELD_FEM_ADRCTRL	59	65	53	16	33	10
5717	G	A	HELD_ALL_ADRCASE5ULN	26	20	32	3	14	9	HELD_ALL_ADRCTRL	132	142	122	39	64	29
5717	G	A	CVD_FEM_CASE	17	12	22	3	6	8	CVD_FEM_CTRL	19	22	16	5	12	2
5850	G	A	HELD_MAL_CASE	14	14	14	5	4	5	HELD_MAL_CTRL	15	21	9	6	9	0
5959	G	A	CVD_MAL_CASE	58	78	38	27	24	7	CVD_MAL_CTRL	29	30	28	6	18	5
6151	C	A	HELD_MAL_ADRCASE	58	76	40	22	32	4	HELD_MAL_ADRCTRL	58	83	33	32	19	7
6236	T	C	HELD_ALL_ADRCASE	129	177	81	67	43	19	HELD_ALL_ADRCTRL	128	193	63	72	49	7
6277	T	G	HELD_FEM_ADRCASE5ULN	16	21	11	8	5	3	HELD_FEM_ADRCTRL	66	112	20	46	20	0
6277	T	G	HELD_ALL_ADRCASE5ULN	23	33	13	13	7	3	HELD_ALL_ADRCTRL	124	205	43	82	41	1
6277	T	G	HELD_FEM_ADRCASE	72	105	39	39	27	6	HELD_FEM_ADRCTRL	66	112	20	46	20	0
6277	T	G	HELD_FEM_ADRCASE3ULN	30	42	18	15	12	3	HELD_FEM_ADRCTRL	66	112	20	46	20	0
6313	C	T	HELD_FEM_UHIRESP	52	54	50	15	24	13	HELD_FEM_ULORESP	72	89	55	23	43	6
6369	T	C	HELD_FEM_BAD	63	82	44	26	30	7	HELD_FEM_GOOD	68	72	64	19	34	15
6374	T	C	HELD_ALL_ADRCASE3ULN	47	52	42	14	24	9	HELD_ALL_ADRCTRL	126	177	75	62	53	11
6374	T	C	HELD_MAL_ADRCASE3ULN	17	15	19	3	9	5	HELD_MAL_ADRCTRL	58	79	37	28	23	7

#dbSNP	A1	A2	COHORT_A	SIZE_A	FQ1_A	FQ2_A	FQ11_A	FQ12_A	FQ22_A	COHORT_B	SIZE_B	FQ1_B	FQ2_B	FQ11_B	FQ12_B	FQ22_B
6396	T	C	HELD_MAL_CASE	14	0	28	14	0	0	HELD_MAL_CTRL	18	30	6	12	6	0
6396	T	C	HELD_ALL_CASE	45	83	7	39	5	1	HELD_ALL_CTRL	40	65	15	26	13	1
6396	T	C	CVD_FEM_CASE	35	55	15	21	13	1	CVD_FEM_CTRL	37	67	7	30	7	0
6396	T	C	CVD_ALL_CASE	97	167	27	72	23	2	CVD_ALL_CTRL	70	130	10	60	10	0
6486	G	A	HELD_ALL_CASE2	86	140	32	59	22	5	HELD_ALL_CTRL2	69	124	14	56	12	1
6520	G	A	HELD_MAL_ADRCASE5ULN	8	11	5	5	1	2	HELD_MAL_ADRCTRL	60	99	21	39	21	0
6520	G	A	HELD_MAL_ADRCASE3ULN	16	23	9	10	3	3	HELD_MAL_ADRCTRL	60	99	21	39	21	0
6520	G	A	HELD_ALL_ADRCASE5ULN	25	35	15	13	9	3	HELD_ALL_ADRCTRL	131	212	50	83	46	2
6520	G	A	HELD_MAL_ADRCASE	62	96	28	39	18	5	HELD_MAL_ADRCTRL	60	99	21	39	21	0
6522	G	A	HELD_FEM_ADRCASE3ULN	31	49	13	18	13	0	HELD_FEM_ADRCTRL	71	121	21	53	15	3
6522	G	A	HELD_FEM_ADRCASE	73	113	33	42	29	2	HELD_FEM_ADRCTRL	71	121	21	53	15	3
6524	A	G	HELD_MAL_ADRCASE3ULN	17	26	8	9	8	0	HELD_MAL_ADRCTRL	59	62	56	13	36	10
6596	C	T	HELD_FEM_ADRCASE3ULN	31	49	13	18	13	0	HELD_FEM_ADRCTRL	71	138	4	67	4	0
6596	C	T	HELD_FEM_ADRCASE5ULN	17	27	7	10	7	0	HELD_FEM_ADRCTRL	71	138	4	67	4	0
6596	C	T	HELD_ALL_ADRCASE3ULN	48	81	15	33	15	0	HELD_ALL_ADRCTRL	131	250	12	119	12	0
6596	C	T	HELD_FEM_ADRCASE	73	127	19	54	19	0	HELD_FEM_ADRCTRL	71	138	4	67	4	0
6596	C	T	HELD_ALL_ADRCASE5ULN	26	44	8	18	8	0	HELD_ALL_ADRCTRL	131	250	12	119	12	0
6596	C	T	HELD_ALL_ADRCASE	136	246	26	110	26	0	HELD_ALL_ADRCTRL	131	250	12	119	12	0
6734	A	C	HELD_ALL_CASE	12	21	3	9	3	0	HELD_ALL_CTRL	15	30	0	15	0	0
6743	G	C	HELD_ALL_ADRCASE	125	153	97	43	67	15	HELD_ALL_ADRCTRL	117	149	85	53	43	21
7128	C	T	HELD_ALL_ADRCASE3ULN	44	75	13	33	9	2	HELD_ALL_ADRCTRL	114	157	71	55	47	12

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1 A	FQ2 A	FQ11 A	FQ12 A	FQ22 A	COHORT_B	SIZE_B	FQ1 B	FQ2 B	FQ11 B	FQ12 B	FQ22 B
7128	C	T	HELD_FEM_ADRCASE3ULN	28	47	9	21	5	2	HELD_FEM_ADRCTRL	59	77	41	25	27	7
7128	C	T	HELD_ALL_ADRCASE5ULN	23	39	7	17	5	1	HELD_ALL_ADRCTRL	114	157	71	55	47	12
7128	C	T	HELD_FEM_ADRCASE	66	101	31	42	17	7	HELD_FEM_ADRCTRL	59	77	41	25	27	7
7128	C	T	HELD_FEM_ADRCASE5ULN	15	25	5	11	3	1	HELD_FEM_ADRCTRL	59	77	41	25	27	7
7363	G	A	HELD_FEM_BAD	81	113	49	39	35	7	HELD_FEM_GOOD	79	127	31	50	27	2
7363	G	A	HELD_ALL_BAD	100	143	57	51	41	8	HELD_ALL_GOOD	115	185	45	73	39	3
7409	A	G	HELD_FEM_ADRCASE5ULN	17	24	10	8	8	1	HELD_FEM_ADRCTRL	72	130	14	58	14	0
7409	A	G	HELD_FEM_ADRCASE3ULN	31	48	14	18	12	1	HELD_FEM_ADRCTRL	72	130	14	58	14	0
7409	A	G	HELD_MAL_ADRCASE5ULN	7	14	0	7	0	0	HELD_MAL_ADRCTRL	59	95	23	39	17	3
8138	T	C	HELD_MAL_BAD	19	28	10	11	6	2	HELD_MAL_GOOD	35	33	37	7	19	9
8138	T	C	HELD_MAL_CASE	14	16	12	3	10	1	HELD_MAL_CTRL	19	18	20	7	4	8
8138	T	C	HELD_ALL_BAD	94	112	76	38	36	20	HELD_ALL_GOOD	114	116	112	28	60	26
8168	C	A	HELD_MAL_BAD	19	28	10	10	8	1	HELD_MAL_GOOD	36	66	6	31	4	1
8168	C	A	HELD_FEM_BAD	79	136	22	61	14	4	HELD_FEM_GOOD	79	125	33	48	29	2
8210	G	A	HELD_ALL_ADRCASE3ULN	46	53	39	19	15	12	HELD_ALL_ADRCTRL	124	147	101	38	71	15
8210	G	A	HELD_FEM_ADRCASE3ULN	29	30	28	10	10	9	HELD_FEM_ADRCTRL	67	78	56	18	42	7
8210	G	A	HELD_FEM_ADRCASE	69	70	68	20	30	19	HELD_FEM_ADRCTRL	67	78	56	18	42	7
8210	G	A	HELD_ALL_ADRCASE	127	137	117	41	55	31	HELD_ALL_ADRCTRL	124	147	101	38	71	15
8241	A	G	HELD_FEM_BAD	76	136	16	60	16	0	HELD_FEM_GOOD	77	120	34	47	26	4
8241	A	G	HELD_ALL_BAD	95	166	24	74	18	3	HELD_ALL_GOOD	112	179	45	74	31	7
8249	C	T	HELD_ALL_ADRCASE3ULN	48	86	10	38	10	0	HELD_ALL_ADRCTRL	129	246	12	117	12	0

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1 A	FQ2 A	FQ11 A	FQ12 A	FQ22 A	COHORT_B	SIZE_B	FQ1 B	FQ2 B	FQ11 B	FQ12 B	FQ22 B
8249	C	T	HELD_ALL_ADRCASE5ULN	26	46	6	20	6	0	HELD_ALL_ADRCTRL	129	246	12	117	12	0
8480	C	G	CVD_FEM_CASE	27	48	6	23	2	2	CVD_FEM_CTRL	39	78	0	39	0	0
8480	C	G	CVD_MAL_CASE	54	99	9	48	3	3	CVD_MAL_CTRL	34	68	0	34	0	0
8577	T	C	HELD_ALL_ADRCASE3ULN	47	50	44	12	26	9	HELD_ALL_ADRCTRL	126	167	85	56	55	15
8577	T	C	HELD_ALL_ADRCASE	132	151	113	41	69	22	HELD_ALL_ADRCTRL	126	167	85	56	55	15
8577	T	C	HELD_ALL_ADRCASE5ULN	26	27	25	7	13	6	HELD_ALL_ADRCTRL	126	167	85	56	55	15
8578	G	A	HELD_ALL_ADRCASE3ULN	48	51	45	12	27	9	HELD_ALL_ADRCTRL	130	169	91	56	57	17
8653	C	T	HELD_MAL_ADRCASE	47	87	7	40	7	0	HELD_MAL_ADRCTRL	52	81	23	29	23	0
8653	C	T	HELD_MAL_ADRCASE3ULN	14	27	1	13	1	0	HELD_MAL_ADRCTRL	52	81	23	29	23	0
8653	C	T	HELD_MAL_ADRCASE5ULN	7	14	0	7	0	0	HELD_MAL_ADRCTRL	52	81	23	29	23	0
8653	C	T	HELD_ALL_ADRCASE3ULN	41	74	8	34	6	1	HELD_ALL_ADRCTRL	114	187	41	74	39	1
8816	G	C	HELD_FEM_BAD2	315	403	227	125	153	37	HELD_FEM_GOOD2	370	419	321	122	175	73
8816	G	C	HELD_FEM_LOHDL	18	24	12	7	10	1	HELD_FEM_HIHDL	22	17	27	2	13	7
8816	G	C	HELD_ALL_CASE2	90	121	59	46	29	15	HELD_ALL_CTRL2	70	78	62	21	36	13
8816	G	C	CVD_ALL_CASE	92	138	46	57	24	11	CVD_ALL_CTRL	65	111	19	51	9	5
8816	G	C	HELD_FEM_CASE2	52	71	33	27	17	8	HELD_FEM_CTRL2	42	44	40	12	20	10
8816	G	C	HELD_MAL_LOHDL	18	22	14	7	8	3	HELD_MAL_HIHDL	17	21	13	4	13	0
8931	C	T	HELD_FEM_ADRCASE3ULN	23	43	3	21	1	1	HELD_FEM_ADRCTRL	42	70	14	29	12	1
8943	A	C	HELD_MAL_ADRCASE3ULN	16	30	2	14	2	0	HELD_MAL_ADRCTRL	55	85	25	33	19	3
9243	C	G	HELD_FEM_VHIRESP	139	230	48	92	46	1	HELD_FEM_VLORESP	143	223	63	89	45	9
9243	C	G	HELD_MAL_ADRCASE5ULN	9	16	2	8	0	1	HELD_MAL_ADRCTRL	60	91	29	35	21	4

baySNP	A1	A2	COHORT_A	SIZE A	FQ1 A	FQ2 A	FQ11 A	FQ12 A	FQ22 A	COHORT_B	SIZE B	FQ1 B	FQ2 B	FQ11 B	FQ12 B	FQ22 B
9243	C	G	HELD_FEM_UHIRESP	54	90	18	36	18	0	HELD_FEM_ULORESP	74	113	35	45	23	6
9523	G	A	HELD_MAL_ADRCASE5ULN	8	12	4	4	4	0	HELD_MAL_ADRCTRL	60	109	11	49	11	0
9940	C	T	HELD_MAL_CASE	12	24	0	12	0	0	HELD_MAL_CTRL	14	23	5	9	5	0
9940	C	T	HELD_ALL_CASE	38	71	5	34	3	1	HELD_ALL_CTRL	31	50	12	20	10	1
10091	T	C	HELD_ALL_ADRCASE3ULN	48	74	22	28	18	2	HELD_ALL_ADRCTRL	129	222	36	94	34	1
10541	G	C	HELD_FEM_UHIRESP	55	103	7	49	5	1	HELD_FEM_ULORESP	77	131	23	55	21	1
10541	G	C	HELD_FEM_VHIRESP	151	283	19	133	17	1	HELD_FEM_VLORESP	145	256	34	113	30	2
10600	G	A	CVD_MAL_CASE	67	0	134	67	0	0	CVD_MAL_CTRL	34	64	4	31	2	1
10600	G	A	HELD_ALL_LOHDL	39	0	78	39	0	0	HELD_ALL_HIHDL	47	88	6	41	6	0
10600	G	A	HELD_MAL_LOHDL	19	0	38	19	0	0	HELD_MAL_HIHDL	23	42	4	19	4	0
10745	G	A	HELD_MAL_BAD	19	32	6	14	4	1	HELD_MAL_GOOD	35	47	23	15	17	3
10748	T	C	HELD_MAL_BAD	13	15	11	4	7	2	HELD_MAL_GOOD	30	47	13	19	9	2
10749	C	G	HELD_FEM_BAD	81	124	38	46	32	3	HELD_FEM_GOOD	77	100	54	32	36	9
10785	T	C	CVD_MAL_CASE	69	128	10	60	8	1	CVD_MAL_CTRL	33	55	11	23	9	1
10811	A	G	HELD_FEM_BAD2	243	382	104	148	86	9	HELD_FEM_GOOD2	300	440	160	154	132	14
10811	A	G	CVD_ALL_CASE	103	155	51	58	39	6	CVD_ALL_CTRL	74	124	24	53	18	3
10830	G	A	HELD_ALL_BAD2	637	723	551	203	317	117	HELD_ALL_GOOD2	725	742	708	201	340	184
10830	G	A	HELD_ALL_BAD	99	113	85	34	45	20	HELD_ALL_GOOD	114	98	130	22	54	38
10830	G	A	HELD_MAL_BAD2	314	357	271	101	155	58	HELD_MAL_GOOD2	347	346	348	88	170	89
10830	G	A	CVD_FEM_CASE	35	44	26	13	18	4	CVD_FEM_CTRL	39	33	45	5	23	11
10830	G	A	HELD_MAL_BAD	19	24	14	7	10	2	HELD_MAL_GOOD	36	29	43	6	17	13

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1 A	FQ2 A	FQ11 A	FQ12 A	FQ22 A	COHORT_B	SIZE_B	FQ1 B	FQ2 B	FQ11 B	FQ12 B	FQ22 B
10830	G	A	HELD_FEM_BAD	80	89	71	27	35	18	HELD_FEM_GOOD	78	69	87	16	37	25
10949	G	C	HELD_FEM_VHIRESP	140	163	117	45	73	22	HELD_FEM_VLORESP	143	191	95	66	59	18
10949	G	C	HELD_FEM_HIRESP	269	319	219	92	135	42	HELD_FEM_LORESP	282	369	195	123	123	36
10962	A	G	CVD_FEM_CASE	18	2	34	0	2	16	CVD_FEM_CTRL	18	9	27	0	9	9
10962	A	G	HELD_ALL_ADRCASE3ULN	47	75	19	28	19	0	HELD_ALL_ADRCTRL	117	173	61	65	43	9
10966	T	C	HELD_ALL_ADRCASE3ULN	47	74	20	27	20	0	HELD_ALL_ADRCTRL	126	179	73	63	53	10
10966	T	C	HELD_ALL_ADRCASE5ULN	25	42	8	17	8	0	HELD_ALL_ADRCTRL	126	179	73	63	53	10
11000	T	C	HELD_MAL_BAD2	313	483	143	187	109	17	HELD_MAL_GOOD2	348	495	201	174	147	27
11000	T	C	CVD_FEM_CASE	35	54	16	20	14	1	CVD_FEM_CTRL	40	62	18	28	6	6
11000	T	C	HELD_MAL_ADRCASE3ULN	17	18	16	4	10	3	HELD_MAL_ADRCTRL	60	87	33	29	29	2
11000	T	C	HELD_ALL_BAD2	630	973	287	375	223	32	HELD_ALL_GOOD2	725	1069	381	390	289	46
11000	T	C	HELD_MAL_ADRCASE5ULN	9	9	9	2	5	2	HELD_MAL_ADRCTRL	60	87	33	29	29	2
11001	T	C	HELD_MAL_BAD2	309	476	142	185	106	18	HELD_MAL_GOOD2	333	471	195	165	141	27
11001	T	C	HELD_ALL_BAD2	620	960	280	372	216	32	HELD_ALL_GOOD2	709	1044	374	381	282	46
11001	T	C	CVD_FEM_CASE	34	52	16	19	14	1	CVD_FEM_CTRL	40	61	19	27	7	6
11001	T	C	HELD_MAL_ADRCASE3ULN	17	18	16	4	10	3	HELD_MAL_ADRCTRL	60	87	33	29	29	2
11001	T	C	HELD_ALL_BAD	102	163	41	64	35	3	HELD_ALL_GOOD	115	165	65	60	45	10
11020	C	T	HELD_MAL_ADRCASE3ULN	15	25	5	10	5	0	HELD_MAL_ADRCTRL	58	76	40	25	26	7
11073	G	C	HELD_FEM_BAD	79	90	68	26	38	15	HELD_FEM_GOOD	78	107	49	37	33	8
11073	G	C	HELD_ALL_CASE2	106	134	78	43	48	15	HELD_ALL_CTRL2	68	100	36	39	22	7
11192	T	A	HELD_FEM_ADRCASE5ULN	16	20	12	8	4	4	HELD_FEM_ADRCTRL	70	101	39	34	33	3

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1 A	FQ2 A	FQ11 A	FQ12 A	FQ22 A	COHORT_B	SIZE_B	FQ1 B	FQ2 B	FQ11 B	FQ12 B	FQ22 B
11192	T	A	HELD_FEM_ADRCASE3ULN	29	37	21	14	9	6	HELD_FEM_ADRCTRL	70	101	39	34	33	3
11248	C	T	HELD_FEM_ADRCASE3ULN	30	51	9	23	5	2	HELD_FEM_ADRCTRL	68	95	41	32	31	5
11248	C	T	HELD_ALL_ADRCASE	131	205	57	81	43	7	HELD_ALL_ADRCTRL	125	176	74	61	54	10
11410	G	T	HELD_FEM_VHIRESP	138	154	122	38	78	22	HELD_FEM_VLORESP	141	137	145	39	59	43
11448	G	A	HELD_MAL_LOHDL	19	21	17	6	9	4	HELD_MAL_HIHDL	25	45	5	21	3	1
11448	G	A	HELD_MAL_BAD	19	25	13	8	9	2	HELD_MAL_GOOD	36	64	8	30	4	2
11448	G	A	HELD_MAL_BAD2	312	478	146	178	122	12	HELD_MAL_GOOD2	344	562	126	234	94	16
11448	G	A	HELD_ALL_BAD2	628	962	294	366	230	32	HELD_ALL_GOOD2	718	1157	279	474	209	35
11448	G	A	HELD_ALL_LOHDL	42	59	25	22	15	5	HELD_ALL_HIHDL	56	95	17	42	11	3
11448	G	A	HELD_FEM_ADRCASE	69	99	39	36	27	6	HELD_FEM_ADRCTRL	68	114	22	48	18	2
11448	G	A	HELD_ALL_ADRCASE	127	190	64	71	48	8	HELD_ALL_ADRCTRL	124	207	41	86	35	3
11448	G	A	HELD_ALL_CASE	44	62	26	22	18	4	HELD_ALL_CTRL	40	66	14	26	14	0
11450	T	A	HELD_MAL_BAD	19	21	17	6	9	4	HELD_MAL_GOOD	36	61	11	27	7	2
11456	A	G	CVD_FEM_CASE	34	59	9	25	9	0	CVD_FEM_CTRL	40	79	1	39	1	0
11462	G	T	HELD_MAL_BAD2	317	566	68	253	60	4	HELD_MAL_GOOD2	350	653	47	304	45	1
11462	G	T	HELD_ALL_BAD2	635	1142	128	515	112	8	HELD_ALL_GOOD2	735	1355	115	622	111	2
11483	T	C	HELD_FEM_ADRCASE5ULN	17	30	4	13	4	0	HELD_FEM_ADRCTRL	69	133	5	65	3	1
11483	T	C	HELD_FEM_ADRCASE3ULN	31	56	6	25	6	0	HELD_FEM_ADRCTRL	69	133	5	65	3	1
11483	T	C	HELD_FEM_ADRCASE	73	135	11	62	11	0	HELD_FEM_ADRCTRL	69	133	5	65	3	1
11531	G	A	HELD_FEM_CASE	31	47	15	21	5	5	HELD_FEM_CTRL	22	41	3	19	3	0
11536	C	G	HELD_ALL_CASE	43	66	20	27	12	4	HELD_ALL_CTRL	40	63	17	23	17	0

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1 A	FQ2 A	FQ11_A	FQ12_A	FQ22_A	COHORT_B	SIZE_B	FQ1 B	FQ2 B	FQ11_B	FQ12_B	FQ22_B
11537	A	G	HELD_MAL_ADRCASE	63	93	33	36	21	6	HELD_MAL_ADRCTRL	60	101	19	43	15	2
11558	A	C	HELD_MAL_BAD2	313	502	124	196	110	7	HELD_MAL_GOOD2	347	596	98	258	80	9
11558	A	C	HELD_ALL_BAD2	633	1036	230	422	192	19	HELD_ALL_GOOD2	722	1239	205	535	169	18
11558	A	C	HELD_ALL_CASE	45	81	9	38	5	2	HELD_ALL_CTRL	40	65	15	26	13	1
11585	G	T	HELD_MAL_CASE	14	22	6	8	6	0	HELD_MAL_CTRL	18	17	19	5	7	6
11594	T	C	HELD_ALL_ADRCASE3ULN	46	91	1	45	1	0	HELD_ALL_ADRCTRL	127	234	20	109	16	2
11594	T	C	HELD_MAL_ADRCASE	61	119	3	58	3	0	HELD_MAL_ADRCTRL	58	106	10	48	10	0
11614	T	C	HELD_FEM_CASE	31	52	10	21	10	0	HELD_FEM_CTRL	22	30	14	12	6	4
11614	T	C	HELD_MAL_CASE2	48	84	12	36	12	0	HELD_MAL_CTRL2	29	43	15	17	9	3
11614	T	C	HELD_ALL_CASE	45	74	16	29	16	0	HELD_ALL_CTRL	40	60	20	24	12	4
11614	T	C	HELD_ALL_LOHDL	45	76	14	35	6	4	HELD_ALL_HIHDL	59	99	19	41	17	1
11631	G	A	HELD_MAL_ADRCASE5ULN	9	8	10	1	6	2	HELD_MAL_ADRCTRL	59	87	31	32	23	4
11631	G	A	HELD_MAL_ADRCASE3ULN	17	19	15	5	9	3	HELD_MAL_ADRCTRL	59	87	31	32	23	4
11637	A	C	HELD_FEM_BAD	77	101	53	36	29	12	HELD_FEM_GOOD	79	121	37	44	33	2
11637	A	C	HELD_ALL_BAD	96	123	69	42	39	15	HELD_ALL_GOOD	114	171	57	63	45	6
11637	A	C	CVD_MAL_CASE	69	111	27	44	23	2	CVD_MAL_CTRL	34	45	23	15	15	4
11637	A	C	CVD_ALL_CASE	105	169	41	67	35	3	CVD_ALL_CTRL	74	104	44	36	32	6
11641	G	C	HELD_MAL_ADRCASE	60	74	46	24	26	10	HELD_MAL_ADRCTRL	57	59	55	10	39	8
11645	G	A	HELD_FEM_CASE	31	60	2	29	2	0	HELD_FEM_CTRL	22	38	6	16	6	0
11646	C	T	HELD_FEM_BAD	81	122	40	48	26	7	HELD_FEM_GOOD	79	102	56	33	36	10
11646	C	T	HELD_ALL_BAD	100	150	50	58	34	8	HELD_ALL_GOOD	115	152	78	49	54	12

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1 A	FQ2 A	FQ11 A	FQ12 A	FQ22 A	COHORT_B	SIZE B	FQ1 B	FQ2 B	FQ11 B	FQ12 B	FQ22 B
11652	C	T	HELD_MAL_BAD	19	22	16	5	12	2	HELD_MAL_GOOD	35	40	30	15	10	10
11727	G	A	HELD_ALL_ADRCASE5ULN	20	0	40	20	0	0	HELD_ALL_ADRCTRL	104	170	38	71	28	5
11727	G	A	HELD_MAL_ADRCASE3ULN	13	0	26	13	0	0	HELD_MAL_ADRCTRL	46	68	24	26	16	4
11727	G	A	HELD_MAL_ADRCASE5ULN	8	0	16	8	0	0	HELD_MAL_ADRCTRL	46	68	24	26	16	4
11727	G	A	HELD_ALL_ADRCASE3ULN	37	70	4	33	4	0	HELD_ALL_ADRCTRL	104	170	38	71	28	5
11727	G	A	HELD_FEM_ADRCASE5ULN	12	0	24	12	0	0	HELD_FEM_ADRCTRL	58	102	14	45	12	1
11728	T	C	HELD_ALL_ADRCASE5ULN	24	44	4	20	4	0	HELD_ALL_ADRCTRL	128	205	51	81	43	4
11914	A	T	HELD_MAL_ADRCASE3ULN	15	10	20	5	0	10	HELD_MAL_ADRCTRL	56	63	49	31	1	24
11938	T	C	HELD_ALL_ADRCASE3ULN	48	64	32	18	28	2	HELD_ALL_ADRCTRL	132	163	101	57	49	26
11938	T	C	HELD_ALL_ADRCASE5ULN	26	33	19	8	17	1	HELD_ALL_ADRCTRL	132	163	101	57	49	26
11938	T	C	HELD_FEM_ADRCASE3ULN	31	38	24	9	20	2	HELD_FEM_ADRCTRL	72	83	61	27	29	16
11950	G	A	HELD_MAL_ADRCASE5ULN	8	0	16	8	0	0	HELD_MAL_ADRCTRL	55	78	32	26	26	3
11950	G	A	HELD_MAL_ADRCASE3ULN	15	27	3	13	1	1	HELD_MAL_ADRCTRL	55	78	32	26	26	3
11950	G	A	HELD_MAL_ADRCASE	55	84	26	35	14	6	HELD_MAL_ADRCTRL	55	78	32	26	26	3
11951	G	A	HELD_MAL_ADRCASE5ULN	7	0	14	7	0	0	HELD_MAL_ADRCTRL	58	84	32	29	26	3
11951	G	A	HELD_FEM_UHIRESP	55	82	28	32	18	5	HELD_FEM_ULORESP	76	127	25	51	25	0
12008	C	T	HELD_ALL_ADRCASE	119	234	4	115	4	0	HELD_ALL_ADRCTRL	113	215	11	102	11	0
12031	A	G	HELD_ALL_ADRCASE3ULN	47	51	43	19	13	15	HELD_ALL_ADRCTRL	126	144	108	37	70	19
12031	A	G	HELD_FEM_ADRCASE5ULN	17	13	21	4	5	8	HELD_FEM_ADRCTRL	70	79	61	18	43	9
12031	A	G	HELD_ALL_ADRCASE5ULN	26	22	30	7	8	11	HELD_ALL_ADRCTRL	126	144	108	37	70	19
12031	A	G	HELD_FEM_ADRCASE3ULN	30	29	31	10	9	11	HELD_FEM_ADRCTRL	70	79	61	18	43	9

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1 A	FQ2 A	FQ11 A	FQ12 A	FQ22 A	COHORT_B	SIZE B	FQ1 B	FQ2 B	FQ11 B	FQ12 B	FQ22 B
12031	A	G	HELD_ALL_ADRCASE	133	133	133	39	55	39	HELD_ALL_ADRCTRL	126	144	108	37	70	19
12031	A	G	HELD_FEM_ADRCASE	72	68	76	19	30	23	HELD_FEM_ADRCTRL	70	79	61	18	43	9
12032	T	C	HELD_FEM_UHIRESP	51	88	14	38	12	1	HELD_FEM_ULORESP	71	136	6	65	6	0
12032	T	C	HELD_FEM_ADRCASE	73	130	16	59	12	2	HELD_FEM_ADRCTRL	70	134	6	64	6	0
12032	T	C	HELD_ALL_ADRCASE	134	240	28	109	22	3	HELD_ALL_ADRCTRL	128	242	14	114	14	0
12032	T	C	HELD_FEM_VHIRESP	136	243	29	108	27	1	HELD_FEM_VLORESP	140	262	18	124	14	2
12148	G	A	HELD_MAL_ADRCASE5ULN	8	7	9	1	5	2	HELD_MAL_ADRCTRL	55	83	27	30	23	2
12148	G	A	HELD_MAL_ADRCASE	55	66	44	19	28	8	HELD_MAL_ADRCTRL	55	83	27	30	23	2
12148	G	A	HELD_MAL_ADRCASE3ULN	16	18	14	5	8	3	HELD_MAL_ADRCTRL	55	83	27	30	23	2
12207	A	G	HELD_MAL_ADRCASE5ULN	9	12	6	6	0	3	HELD_MAL_ADRCTRL	58	84	32	29	26	3
12207	A	G	HELD_MAL_ADRCASE	59	74	44	30	14	15	HELD_MAL_ADRCTRL	58	84	32	29	26	3
12207	A	G	HELD_MAL_ADRCASE3ULN	17	23	11	10	3	4	HELD_MAL_ADRCTRL	58	84	32	29	26	3
12399	A	G	HELD_MAL_ADRCASE5ULN	8	11	5	3	5	0	HELD_MAL_ADRCTRL	60	106	14	46	14	0
12399	A	G	HELD_MAL_ADRCASE3ULN	16	24	8	8	8	0	HELD_MAL_ADRCTRL	60	106	14	46	14	0
12399	A	G	HELD_ALL_ADRCASE	132	217	47	89	39	4	HELD_ALL_ADRCTRL	131	232	30	103	26	2
12554	A	T	HELD_MAL_ADRCASE	62	98	26	37	24	1	HELD_MAL_ADRCTRL	55	99	11	44	11	0
12554	A	T	HELD_FEM_VHIRESP	151	234	68	88	58	5	HELD_FEM_VLORESP	144	243	45	102	39	3
12851	T	C	HELD_FEM_ADRCASE5ULN	17	22	12	6	10	1	HELD_FEM_ADRCTRL	71	115	27	46	23	2
12851	T	C	HELD_MAL_ADRCASE	62	94	30	34	26	2	HELD_MAL_ADRCTRL	60	88	32	36	16	8
13025	A	C	HELD_MAL_ADRCASE3ULN	17	24	10	11	2	4	HELD_MAL_ADRCTRL	58	80	36	28	24	6
13025	A	C	HELD_FEM_ADRCASE5ULN	17	19	15	7	5	5	HELD_FEM_ADRCTRL	70	93	47	29	35	6

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1_A	FQ2_A	FQ11_A	FQ12_A	FQ22_A	COHORT_B	SIZE_B	FQ1_B	FQ2_B	FQ11_B	FQ12_B	FQ22_B
13191	G	A	HELD_ALL_CASE	43	50	36	16	18	9	HELD_ALL_CTRL	39	58	20	21	16	2
13192	T	C	HELD_MAL_ADRCASE3ULN	17	25	9	11	3	3	HELD_MAL_ADRCTRL	59	97	21	38	21	0
13192	T	C	HELD_MAL_ADRCASE5ULN	9	14	4	6	2	1	HELD_MAL_ADRCTRL	59	97	21	38	21	0
13192	T	C	HELD_ALL_ADRCASE3ULN	47	77	17	33	11	3	HELD_ALL_ADRCTRL	129	212	46	84	44	1
13192	T	C	HELD_MAL_ADRCASE	61	98	24	41	16	4	HELD_MAL_ADRCTRL	59	97	21	38	21	0
13193	G	A	HELD_MAL_ADRCASE3ULN	16	23	9	10	3	3	HELD_MAL_ADRCTRL	58	94	22	36	22	0
13193	G	A	HELD_MAL_ADRCASE5ULN	8	12	4	5	2	1	HELD_MAL_ADRCTRL	58	94	22	36	22	0
13193	G	A	HELD_ALL_ADRCASE3ULN	47	77	17	33	11	3	HELD_ALL_ADRCTRL	130	212	48	83	46	1
13338	G	A	HELD_FEM_UHIRESP	55	75	35	23	29	3	HELD_FEM_ULORESP	71	92	50	34	24	13
13338	G	A	HELD_FEM_VHIRESP	148	187	109	58	71	19	HELD_FEM_VLORESP	139	178	100	66	46	27
13339	G	A	HELD_MAL_ADRCASE	50	42	58	0	42	8	HELD_MAL_ADRCTRL	50	47	53	6	35	9
13339	G	A	CVD_FEM_CASE	31	57	5	26	5	0	CVD_FEM_CTRL	35	56	14	22	12	1
13340	C	A	HELD_FEM_VHIRESP	21	21	21	4	13	4	HELD_FEM_VLORESP	17	27	7	11	5	1
13479	G	A	HELD_FEM_UHIRESP	48	73	23	28	17	3	HELD_FEM_ULORESP	65	113	17	50	13	2
13633	T	C	HELD_FEM_ADRCASE3ULN	27	36	18	12	12	3	HELD_FEM_ADRCTRL	69	112	26	45	22	2
13633	T	C	HELD_FEM_ADRCASE	64	90	38	32	26	6	HELD_FEM_ADRCTRL	69	112	26	45	22	2
13929	G	A	HELD_MAL_ADRCASE5ULN	8	0	16	8	0	0	HELD_MAL_ADRCTRL	54	94	14	41	12	1
14065	C	T	HELD_FEM_HIRESP	267	473	61	208	57	2	HELD_FEM_LORESP	271	501	41	231	39	1
14083	T	C	HELD_FEM_ADRCASE	69	123	15	54	15	0	HELD_FEM_ADRCTRL	70	112	28	46	20	4
14085	T	C	HELD_FEM_HIRESP	240	405	75	168	69	3	HELD_FEM_LORESP	230	404	56	180	44	6
14087	T	C	HELD_FEM_HIRESP	268	452	84	188	76	4	HELD_FEM_LORESP	283	496	70	220	56	7

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1_A	FQ2_A	FQ11_A	FQ12_A	FQ22_A	COHORT_B	SIZE_B	FQ1_B	FQ2_B	FQ11_B	FQ12_B	FQ22_B
14102	C	T	HELD_MAL_ADRCASE5ULN	9	12	6	6	0	3	HELD_MAL_ADRCTRL	56	72	40	21	30	5
14102	C	T	HELD_FEM_HIRESP	271	361	181	123	115	33	HELD_FEM_LORESP	281	340	222	107	126	48
14103	C	T	HELD_FEM_HIRESP	264	445	83	192	61	11	HELD_FEM_LORESP	273	482	64	209	64	0
14103	C	T	HELD_FEM_VHIRESP	137	234	40	103	28	6	HELD_FEM_VLORESP	135	236	34	101	34	0
14103	C	T	HELD_FEM_UHIRESP	53	84	22	35	14	4	HELD_FEM_ULORESP	69	121	17	52	17	0
14129	A	G	HELD_ALL_ADRCASE3ULN	47	53	41	18	17	12	HELD_ALL_ADRCTRL	116	151	81	47	57	12
14129	A	G	HELD_MAL_ADRCASE3ULN	16	18	14	7	4	5	HELD_MAL_ADRCTRL	55	72	38	22	28	5
14326	A	C	HELD_FEM_HIRESP	272	454	90	191	72	9	HELD_FEM_LORESP	285	449	121	181	87	17
14503	C	T	HELD_ALL_ADRCASE5ULN	24	34	14	16	2	6	HELD_ALL_ADRCTRL	114	154	74	53	48	13
14503	C	T	HELD_ALL_ADRCASE3ULN	45	58	32	25	8	12	HELD_ALL_ADRCTRL	114	154	74	53	48	13
14503	C	T	HELD_FEM_ADRCASE5ULN	16	21	11	10	1	5	HELD_FEM_ADRCTRL	57	75	39	25	25	7
14503	C	T	HELD_FEM_ADRCASE3ULN	29	35	23	15	5	9	HELD_FEM_ADRCTRL	57	75	39	25	25	7
14537	C	T	HELD_ALL_ADRCASE	118	133	103	38	57	23	HELD_ALL_ADRCTRL	113	156	70	52	52	9
14537	C	T	HELD_FEM_ADRCASE	67	68	66	18	32	17	HELD_FEM_ADRCTRL	59	76	42	22	32	5
15915	T	C	HELD_FEM_ADRCASE	63	95	31	34	27	2	HELD_FEM_ADRCTRL	55	80	30	35	10	10
15915	T	C	HELD_ALL_ADRCASE	111	172	50	65	42	4	HELD_ALL_ADRCTRL	106	158	54	67	24	15
15915	T	C	HELD_ALL_ADRCASE3ULN	38	66	10	29	8	1	HELD_ALL_ADRCTRL	106	158	54	67	24	15
19289	G	A	HELD_MAL_CASE	12	20	4	8	4	0	HELD_MAL_CTRL	18	34	2	17	0	1
19289	G	A	HELD_ALL_CASE	43	71	15	28	15	0	HELD_ALL_CTRL	40	73	7	34	5	1
19289	G	A	HELD_MAL_BAD	19	27	11	9	9	1	HELD_MAL_GOOD	34	59	9	25	9	0
36958	C	G	HELD_MAL_ADRCASE3ULN	15	30	0	15	0	0	HELD_MAL_ADRCTRL	57	104	10	47	10	0

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1_A	FQ2_A	FQ11_A	FQ12_A	FQ22_A	COHORT_B	SIZE_B	FQ1_B	FQ2_B	FQ11_B	FQ12_B	FQ22_B
37158	C	A	HELD_ALL_ADRCASE	122	139	105	40	59	23	HELD_ALL_ADRCTRL	114	157	71	53	51	10
37158	C	A	HELD_FEM_ADRCASE	66	70	62	18	34	14	HELD_FEM_ADRCTRL	58	77	39	23	31	4
37160	C	T	HELD_FEM_UHIRESP	53	86	20	36	14	3	HELD_FEM_ULORESP	73	133	13	60	13	0
37412	T	G	HELD_FEM_ADRCASE5ULN	17	19	15	3	13	1	HELD_FEM_ADRCTRL	69	98	40	35	28	6
37412	T	G	HELD_ALL_ADRCASE5ULN	26	32	20	7	18	1	HELD_ALL_ADRCTRL	129	185	73	65	55	9
37412	T	G	HELD_FEM_ADRCASE3ULN	31	35	27	10	15	6	HELD_FEM_ADRCTRL	69	98	40	35	28	6
37457	T	A	CVD_ALL_CASE	53	101	5	48	5	0	CVD_ALL_CTRL	28	43	13	18	7	3
37457	T	A	CVD_FEM_CASE	17	33	1	16	1	0	CVD_FEM_CTRL	18	27	9	11	5	2
37457	T	A	CVD_MAL_CASE	36	68	4	32	4	0	CVD_MAL_CTRL	10	16	4	7	2	1
37704	C	T	HELD_MAL_ADRCASE5ULN	9	17	1	8	1	0	HELD_MAL_ADRCTRL	60	120	0	60	0	0
38959	C	A	CVD_ALL_CASE	57	99	15	42	15	0	CVD_ALL_CTRL	31	55	7	26	3	2
38959	C	A	HELD_FEM_HIRESP	282	526	38	244	38	0	HELD_FEM_LORESP	280	508	52	232	44	4
39292	G	A	HELD_FEM_ADRCASE5ULN	9	12	6	5	2	2	HELD_FEM_ADRCTRL	47	82	12	36	10	1
39292	G	A	HELD_ALL_ADRCASE5ULN	17	26	8	11	4	2	HELD_ALL_ADRCTRL	86	153	19	70	13	3
39698	T	C	HELD_MAL_ADRCASE3ULN	16	13	19	1	11	4	HELD_MAL_ADRCTRL	56	60	52	19	22	15
39756	T	C	HELD_FEM_ADRCASE3ULN	19	29	9	13	3	3	HELD_FEM_ADRCTRL	44	51	37	19	13	12
39951	T	C	HELD_MAL_ADRCASE	52	78	26	26	26	0	HELD_MAL_ADRCTRL	54	72	36	26	20	8
39951	T	C	HELD_ALL_ADRCASE	117	161	73	48	65	4	HELD_ALL_ADRCTRL	113	159	67	59	41	13
39951	T	C	HELD_FEM_ADRCASE	65	83	47	22	39	4	HELD_FEM_ADRCTRL	59	87	31	33	21	5
39951	T	C	HELD_FEM_ADRCASE5ULN	14	15	13	3	9	2	HELD_FEM_ADRCTRL	59	87	31	33	21	5
40466	G	T	HELD_FEM_HIRESP	266	469	63	204	61	1	HELD_FEM_LORESP	266	436	96	183	70	13

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1 A	FQ2 A	FQ11 A	FQ12 A	FQ22 A	COHORT_B	SIZE_B	FQ1 B	FQ2 B	FQ11 B	FQ12 B	FQ22 B
40466	G	T	HELD_FEM_UHIRESP	52	93	11	41	11	0	HELD_FEM_ULORESP	69	110	28	47	16	6
40466	G	T	HELD_FEM_VHIRESP	139	244	34	106	32	1	HELD_FEM_VLORESP	135	219	51	91	37	7
44442	A	G	HELD_MAL_ADRCASE5ULN	9	8	10	1	6	2	HELD_MAL_ADRCTRL	59	82	36	27	28	4
55504	T	C	HELD_MAL_ADRCASE	60	75	45	23	29	8	HELD_MAL_ADRCTRL	56	54	58	15	24	17
55542	C	A	HELD_FEM_ADRCASE	65	62	68	16	30	19	HELD_FEM_ADRCTRL	69	85	53	24	37	8
55670	C	T	HELD_FEM_VHIRESP	154	297	11	143	11	0	HELD_FEM_VLORESP	138	254	22	116	22	0
55736	A	G	HELD_ALL_ADRCASE5ULN	15	30	0	15	0	0	HELD_ALL_ADRCTRL	87	147	27	62	23	2
55736	A	G	HELD_MAL_ADRCASE5ULN	7	14	0	7	0	0	HELD_MAL_ADRCTRL	43	71	15	28	15	0
55736	A	G	HELD_FEM_ADRCASE5ULN	8	16	0	8	0	0	HELD_FEM_ADRCTRL	44	76	12	34	8	2
55748	T	C	HELD_MAL_ADRCASE5ULN	8	0	16	8	0	0	HELD_MAL_ADRCTRL	56	98	14	43	12	1
55813	T	C	HELD_ALL_ADRCASE3ULN	44	39	49	9	21	14	HELD_ALL_ADRCTRL	119	139	99	44	51	24
55845	C	A	HELD_FEM_VHIRESP	136	152	120	40	72	24	HELD_FEM_VLORESP	135	179	91	61	57	17
55845	C	A	HELD_MAL_ADRCASE3ULN	16	25	7	9	7	0	HELD_MAL_ADRCTRL	58	68	48	18	32	8
55845	C	A	HELD_FEM_UHIRESP	52	58	46	16	26	10	HELD_FEM_ULORESP	68	93	43	32	29	7
55923	C	T	HELD_FEM_ADRCASE	59	63	55	16	31	12	HELD_FEM_ADRCTRL	57	78	36	26	26	5
55923	C	T	HELD_FEM_ADRCASE3ULN	27	27	27	7	13	7	HELD_FEM_ADRCTRL	57	78	36	26	26	5
55945	G	A	HELD_FEM_ADRCASE	66	70	62	18	34	14	HELD_FEM_ADRCTRL	65	92	38	32	28	5
55945	G	A	HELD_FEM_ADRCASE3ULN	28	29	27	8	13	7	HELD_FEM_ADRCTRL	65	92	38	32	28	5
55945	G	A	HELD_ALL_ADRCASE	124	142	106	43	56	25	HELD_ALL_ADRCTRL	122	163	81	54	55	13
56007	T	C	HELD_MAL_ADRCASE3ULN	17	26	8	13	0	4	HELD_MAL_ADRCTRL	49	63	35	24	15	10
56007	T	C	HELD_MAL_ADRCASE5ULN	9	14	4	7	0	2	HELD_MAL_ADRCTRL	49	63	35	24	15	10

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1A	FQ2A	FQ11_A	FQ12_A	FQ22_A	COHORT_B	SIZE_B	FQ1_B	FQ2_B	FQ11_B	FQ12_B	FQ22_B
56011	A	G	HELD_ALL_ADRCASE5ULN	24	48	0	24	0	0	HELD_ALL_ADRCTRL	120	228	12	108	12	0
56104	G	A	HELD_FEM_UHIRESP	56	62	50	18	26	12	HELD_FEM_ULORESP	76	106	46	34	38	4
56113	G	T	HELD_ALL_ADRCASE5ULN	24	20	28	7	6	11	HELD_ALL_ADRCTRL	114	133	95	41	51	22
56113	G	T	HELD_ALL_ADRCASE3ULN	45	47	43	18	11	16	HELD_ALL_ADRCTRL	114	133	95	41	51	22
56113	G	T	HELD_FEM_ADRCASE5ULN	17	13	21	4	5	8	HELD_FEM_ADRCTRL	58	68	48	20	28	10
56113	G	T	HELD_FEM_ADRCASE3ULN	30	28	32	10	8	12	HELD_FEM_ADRCTRL	58	68	48	20	28	10
56636	T	C	HELD_FEM_ADRCASE	70	72	68	23	26	21	HELD_FEM_ADRCTRL	59	65	53	14	37	8
56636	T	C	HELD_FEM_ADRCASE3ULN	31	36	26	13	10	8	HELD_FEM_ADRCTRL	59	65	53	14	37	8
56636	T	C	HELD_FEM_ADRCASE5ULN	18	19	17	7	5	6	HELD_FEM_ADRCTRL	59	65	53	14	37	8
56666	G	A	HELD_MAL_ADRCASE3ULN	13	0	26	13	0	0	HELD_MAL_ADRCTRL	55	89	21	44	1	10
56666	G	A	HELD_MAL_ADRCASE5ULN	8	0	16	8	0	0	HELD_MAL_ADRCTRL	55	89	21	44	1	10
56666	G	A	HELD_MAL_ADRCASE	51	94	8	47	0	4	HELD_MAL_ADRCTRL	55	89	21	44	1	10
56667	T	C	HELD_FEM_HIRESP	264	342	186	108	126	30	HELD_FEM_LORESP	265	304	226	88	128	49
56667	T	C	HELD_MAL_ADRCASE3ULN	17	28	6	14	0	3	HELD_MAL_ADRCTRL	56	71	41	35	1	20
56667	T	C	HELD_FEM_ADRCASE3ULN	30	29	31	6	17	7	HELD_FEM_ADRCTRL	67	85	49	27	31	9
56780	G	A	HELD_FEM_ADRCASE3ULN	26	19	33	1	17	8	HELD_FEM_ADRCTRL	50	58	42	14	30	6
56780	G	A	HELD_FEM_ADRCASE	62	51	73	9	33	20	HELD_FEM_ADRCTRL	50	58	42	14	30	6
56780	G	A	HELD_ALL_ADRCASE3ULN	36	28	44	3	22	11	HELD_ALL_ADRCTRL	94	105	83	26	53	15
56780	G	A	HELD_ALL_ADRCASE	105	96	114	21	54	30	HELD_ALL_ADRCTRL	94	105	83	26	53	15
56876	T	C	HELD_FEM_UHIRESP	57	106	8	50	6	1	HELD_FEM_ULORESP	74	123	25	51	21	2
56876	T	C	HELD_FEM_HIRESP	285	524	46	243	38	4	HELD_FEM_LORESP	274	480	68	211	58	5

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1_A	FQ2_A	FQ11_A	FQ12_A	FQ22_A	COHORT_B	SIZE_B	FQ1_B	FQ2_B	FQ11_B	FQ12_B	FQ22_B
56876	T	C	HELD_FEM_VHIRESP	154	285	23	132	21	1	HELD_FEM_VLORESP	143	248	38	108	32	3
56978	A	G	HELD_ALL_ADRCASE5ULN	26	42	10	17	8	1	HELD_ALL_ADRCTRL	124	157	91	53	51	20
57000	A	T	HELD_FEM_VHIRESP	150	206	94	68	70	12	HELD_FEM_VLORESP	143	206	80	81	44	18
57000	A	T	HELD_FEM_UHIRESP	54	76	32	25	26	3	HELD_FEM_ULORESP	75	104	46	41	22	12
57000	A	T	CVD_ALL_CASE	57	91	23	35	21	1	CVD_ALL_CTRL	32	43	21	16	11	5
57000	A	T	CVD_MAL_CASE	39	64	14	25	14	0	CVD_MAL_CTRL	13	18	8	7	4	2
57313	T	C	HELD_FEM_UHIRESP	55	65	45	23	19	13	HELD_FEM_ULORESP	76	104	48	34	36	6
57734	C	G	HELD_FEM_ADRCASE3ULN	30	45	15	17	11	2	HELD_FEM_ADRCTRL	67	116	18	51	14	2
57837	A	G	HELD_MAL_ADRCASE3ULN	15	28	2	13	2	0	HELD_MAL_ADRCTRL	53	83	23	33	17	3
57853	T	C	HELD_FEM_HIRESP	265	457	73	194	69	2	HELD_FEM_LORESP	265	425	105	176	73	16
57853	T	C	HELD_FEM_UHIRESP	52	91	13	39	13	0	HELD_FEM_ULORESP	68	104	32	43	18	7
57853	T	C	HELD_FEM_VHIRESP	139	238	40	100	38	1	HELD_FEM_VLORESP	135	214	56	87	40	8
57854	G	A	HELD_FEM_HIRESP	267	451	83	187	77	3	HELD_FEM_LORESP	262	420	104	172	76	14
57854	G	A	HELD_FEM_UHIRESP	52	90	14	38	14	0	HELD_FEM_ULORESP	68	104	32	42	20	6
57854	G	A	HELD_MAL_ADRCASE3ULN	16	29	3	13	3	0	HELD_MAL_ADRCTRL	57	86	28	33	20	4
58295	A	G	HELD_MAL_ADRCASE	56	48	64	13	22	21	HELD_MAL_ADRCTRL	54	60	48	14	32	8
58402	T	C	HELD_MAL_ADRCASE3ULN	17	10	24	5	0	12	HELD_MAL_ADRCTRL	56	57	55	28	1	27
58407	G	T	HELD_FEM_VHIRESP	153	195	111	59	77	17	HELD_FEM_VLORESP	145	180	110	65	50	30
58407	G	T	HELD_FEM_UHIRESP	56	76	36	23	30	3	HELD_FEM_ULORESP	76	91	61	31	29	16
58440	T	C	HELD_FEM_UHIRESP	52	81	23	32	17	3	HELD_FEM_ULORESP	72	127	17	56	15	1
58525	C	T	HELD_FEM_ADRCASE	66	110	22	47	16	3	HELD_FEM_ADRCTRL	66	128	4	63	2	1

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1 A	FQ2 A	FQ11 A	FQ12 A	FQ22 A	COHORT_B	SIZE_B	FQ1 B	FQ2 B	FQ11 B	FQ12 B	FQ22 B
58525	C	T	HELD_FEM_ADRCASE3ULN	30	49	11	20	9	1	HELD_FEM_ADRCTRL	66	128	4	63	2	1
58525	C	T	HELD_FEM_ADRCASE5ULN	16	26	6	10	6	0	HELD_FEM_ADRCTRL	66	128	4	63	2	1
58525	C	T	HELD_ALL_ADRCASE	124	212	36	94	24	6	HELD_ALL_ADRCTRL	122	228	16	108	12	2
58525	C	T	HELD_ALL_ADRCASE5ULN	25	42	8	17	8	0	HELD_ALL_ADRCTRL	122	228	16	108	12	2
58525	C	T	HELD_ALL_ADRCASE3ULN	47	80	14	34	12	1	HELD_ALL_ADRCTRL	122	228	16	108	12	2
58533	C	T	HELD_FEM_ADRCASE	67	114	20	50	14	3	HELD_FEM_ADRCTRL	71	136	6	66	4	1
58533	C	T	HELD_FEM_ADRCASE3ULN	27	46	8	20	6	1	HELD_FEM_ADRCTRL	71	136	6	66	4	1
58533	C	T	HELD_FEM_ADRCASE5ULN	14	24	4	10	4	0	HELD_FEM_ADRCTRL	71	136	6	66	4	1
58533	C	T	HELD_ALL_ADRCASE	125	217	33	98	21	6	HELD_ALL_ADRCTRL	129	238	20	112	14	3
58544	G	A	HELD_MAL_ADRCASE5ULN	6	0	12	6	0	0	HELD_MAL_ADRCTRL	54	85	23	35	15	4
58716	T	C	HELD_MAL_ADRCASE3ULN	16	30	2	15	0	1	HELD_MAL_ADRCTRL	59	76	42	38	0	21
58716	T	C	HELD_MAL_ADRCASE5ULN	8	14	2	7	0	1	HELD_MAL_ADRCTRL	59	76	42	38	0	21
58736	C	T	HELD_FEM_HIRESP	289	395	183	139	117	33	HELD_FEM_LORESP	281	344	218	106	132	43
58808	A	G	HELD_FEM_ADRCASE	68	100	36	38	24	6	HELD_FEM_ADRCTRL	61	74	48	22	30	9
58809	C	A	HELD_MAL_ADRCASE5ULN	9	0	18	9	0	0	HELD_MAL_ADRCTRL	59	96	22	40	16	3
58809	C	A	HELD_ALL_ADRCASE3ULN	46	70	22	31	8	7	HELD_ALL_ADRCTRL	128	215	41	91	33	4
58809	C	A	HELD_MAL_ADRCASE3ULN	16	23	9	11	1	4	HELD_MAL_ADRCTRL	59	96	22	40	16	3
58809	C	A	HELD_FEM_UHIRESP	54	94	14	40	14	0	HELD_FEM_ULORESP	75	116	34	44	28	3
58886	A	G	HELD_FEM_ADRCASE3ULN	31	20	42	3	14	14	HELD_FEM_ADRCTRL	72	74	70	19	36	17
58886	A	G	HELD_ALL_ADRCASE3ULN	48	38	58	7	24	17	HELD_ALL_ADRCTRL	132	142	122	39	64	29
58886	A	G	HELD_ALL_ADRCASE5ULN	26	20	32	3	14	9	HELD_ALL_ADRCTRL	132	142	122	39	64	29

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1_A	FQ2_A	FQ11_A	FQ12_A	FQ22_A	COHORT_B	SIZE_B	FQ1_B	FQ2_B	FQ11_B	FQ12_B	FQ22_B
58926	C	T	HELD_MAL_ADRCASE3ULN	15	12	18	2	8	5	HELD_MAL_ADRCTRL	54	75	33	27	21	6
58926	C	T	HELD_ALL_ADRCASE5ULN	22	19	25	4	11	7	HELD_ALL_ADRCTRL	113	144	82	48	48	17
58926	C	T	CVD_FEM_CASE	18	21	15	8	5	5	CVD_FEM_CTRL	19	21	17	4	13	2
58926	C	T	HELD_MAL_ADRCASE5ULN	8	7	9	1	5	2	HELD_MAL_ADRCTRL	54	75	33	27	21	6
58968	A	G	HELD_ALL_ADRCASE5ULN	22	21	23	6	9	7	HELD_ALL_ADRCTRL	118	168	68	70	28	20
58968	A	G	HELD_MAL_ADRCASE3ULN	13	12	14	3	6	4	HELD_MAL_ADRCTRL	55	81	29	34	13	8
58968	A	G	HELD_ALL_ADRCASE3ULN	41	47	35	17	13	11	HELD_ALL_ADRCTRL	118	168	68	70	28	20
58968	A	G	HELD_FEM_ADRCASE5ULN	14	13	15	4	5	5	HELD_FEM_ADRCTRL	63	87	39	36	15	12
58985	G	A	HELD_ALL_ADRCASE5ULN	26	28	24	8	12	6	HELD_ALL_ADRCTRL	130	188	72	69	50	11
59113	C	G	HELD_MAL_ADRCASE5ULN	8	2	14	1	0	7	HELD_MAL_ADRCTRL	55	64	46	32	0	23
59113	C	G	HELD_MAL_ADRCASE3ULN	16	10	22	5	0	11	HELD_MAL_ADRCTRL	55	64	46	32	0	23
59236	G	A	HELD_ALL_ADRCASE	95	103	87	34	35	26	HELD_ALL_ADRCTRL	96	122	70	37	48	11
59236	G	A	HELD_ALL_ADRCASE3ULN	34	39	29	15	9	10	HELD_ALL_ADRCTRL	96	122	70	37	48	11
59236	G	A	HELD_FEM_ADRCASE	52	47	57	15	17	20	HELD_FEM_ADRCTRL	51	59	43	16	27	8
59237	C	T	HELD_FEM_VHIRESP	121	140	102	36	68	17	HELD_FEM_VLORESP	119	138	100	46	46	27
59237	C	T	HELD_FEM_HIRESP	240	290	190	84	122	34	HELD_FEM_LORESP	243	285	201	94	97	52
59267	T	C	HELD_FEM_UHIRESP	50	52	48	17	18	15	HELD_FEM_ULORESP	68	96	40	31	34	3
59352	T	C	HELD_MAL_ADRCASE	58	73	43	18	37	3	HELD_MAL_ADRCTRL	56	74	38	26	22	8
59352	T	C	HELD_ALL_ADRCASE	126	167	85	48	71	7	HELD_ALL_ADRCTRL	125	164	86	55	54	16
59363	T	C	CVD_MAL_CASE	60	84	36	31	22	7	CVD_MAL_CTRL	28	30	26	11	8	9
59368	T	C	HELD_FEM_ADRCASE	66	74	58	23	28	15	HELD_FEM_ADRCTRL	69	100	38	35	30	4

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1-A	FQ2 A	FQ11 A	FQ12 A	FQ22 A	COHORT_B	SIZE_B	FQ1-B	FQ2-B	FQ11 B	FQ12 B	FQ22 B
59371	C	T	HELD_FEM_VHIRESP	141	153	129	48	57	36	HELD_FEM_VLORESP	136	164	108	43	78	15
59371	C	T	HELD_FEM_UHIRESP	52	60	44	22	16	14	HELD_FEM_ULORESP	68	88	48	26	36	6
59372	C	T	HELD_MAL_ADRCASE	55	87	23	38	11	6	HELD_MAL_ADRCTRL	58	104	12	48	8	2
59372	C	T	HELD_MAL_ADRCASE3ULN	17	26	8	11	4	2	HELD_MAL_ADRCTRL	58	104	12	48	8	2
59443	T	C	HELD_ALL_ADRCASE5ULN	19	25	13	11	3	5	HELD_ALL_ADRCTRL	95	110	80	27	56	12
59443	T	C	HELD_MAL_ADRCASE5ULN	7	7	7	3	1	3	HELD_MAL_ADRCTRL	45	47	43	9	29	7
900080	G	C	HELD_FEM_ADRCASE3ULN	31	52	10	22	8	1	HELD_FEM_ADRCTRL	71	135	7	65	5	1
900080	G	C	HELD_FEM_ADRCASE5ULN	17	29	5	12	5	0	HELD_FEM_ADRCTRL	71	135	7	65	5	1
900102	T	G	HELD_FEM_UHIRESP	55	73	37	26	21	8	HELD_FEM_ULORESP	78	76	80	17	42	19
900102	T	G	HELD_FEM_VHIRESP	153	204	102	69	66	18	HELD_FEM_VLORESP	147	168	126	46	76	25
900111	G	A	HELD_FEM_UHIRESP	55	73	37	26	21	8	HELD_FEM_ULORESP	78	79	77	19	41	18
900111	G	A	HELD_FEM_VHIRESP	151	198	104	66	66	19	HELD_FEM_VLORESP	146	166	126	44	78	24
900117	T	G	HELD_MAL_BAD	17	31	3	14	3	0	HELD_MAL_GOOD	33	44	22	16	12	5
900118	G	A	HELD_FEM_HIRESP	252	469	35	219	31	2	HELD_FEM_LORESP	259	444	74	193	58	8
900118	G	A	HELD_FEM_VHIRESP	130	241	19	113	15	2	HELD_FEM_VLORESP	130	225	35	100	25	5
900118	G	A	HELD_FEM_ADRCASE5ULN	15	28	2	14	0	1	HELD_FEM_ADRCTRL	59	109	9	50	9	0
900118	G	A	HELD_ALL_ADRCASE5ULN	23	42	4	21	0	2	HELD_ALL_ADRCTRL	110	205	15	97	11	2
900120	T	C	HELD_FEM_HIRESP	286	511	61	228	55	3	HELD_FEM_LORESP	280	471	89	206	59	15
900121	T	G	HELD_FEM_HIRESP	269	353	185	120	113	36	HELD_FEM_LORESP	266	379	153	134	111	21
900123	A	G	HELD_ALL_ADRCASE	119	238	0	119	0	0	HELD_ALL_ADRCTRL	115	226	4	111	4	0
900123	A	G	HELD_FEM_ADRCASE	64	128	0	64	0	0	HELD_FEM_ADRCTRL	59	115	3	56	3	0

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1A	FQ2A	FQ11_A	FQ12_A	FQ22_A	COHORT_B	SIZE_B	FQ1B	FQ2B	FQ11_B	FQ12_B	FQ22_B
900124	G	A	HELD_FEM_HIRESP	249	254	244	31	192	26	HELD_FEM_LORESP	253	288	218	55	178	20
900132	T	C	HELD_FEM_ADRCASE	67	111	23	44	23	0	HELD_FEM_ADRCTRL	58	89	27	37	15	6
900144	A	G	CVD_FEM_CASE	28	56	0	28	0	0	CVD_FEM_CTRL	40	74	6	34	6	0
900144	A	G	HELD_ALL_ADRCASE5ULN	26	52	0	26	0	0	HELD_ALL_ADRCTRL	125	240	10	115	10	0
900145	G	T	CVD_FEM_CASE	30	58	2	29	0	1	CVD_FEM_CTRL	39	73	5	34	5	0
900145	G	T	HELD_ALL_ADRCASE5ULN	25	50	0	25	0	0	HELD_ALL_ADRCTRL	121	232	10	111	10	0
900146	A	G	HELD_FEM_ADRCASE5ULN	17	22	12	7	8	2	HELD_FEM_ADRCTRL	67	109	25	42	25	0
900146	A	G	HELD_FEM_CASE	30	50	10	20	10	0	HELD_FEM_CTRL	22	34	10	15	4	3
900146	A	G	HELD_MAL_ADRCASE	58	97	19	39	19	0	HELD_MAL_ADRCTRL	54	84	24	34	16	4
900147	T	C	HELD_ALL_ADRCASE3ULN	44	74	14	31	12	1	HELD_ALL_ADRCTRL	119	168	70	61	46	12
900147	T	C	HELD_FEM_ADRCASE3ULN	28	48	8	21	6	1	HELD_FEM_ADRCTRL	66	91	41	31	29	6
900196	C	T	HELD_MAL_BAD	19	17	21	5	7	7	HELD_MAL_GOOD	32	47	17	20	7	5
900196	C	T	HELD_FEM_BAD	12	19	5	8	3	1	HELD_FEM_GOOD	36	37	35	8	21	7
900196	C	T	HELD_FEM_ADRCASE3ULN	23	37	9	14	9	0	HELD_FEM_ADRCTRL	62	77	47	24	29	9
900196	C	T	CVD_FEM_CASE	6	8	4	2	4	0	CVD_FEM_CTRL	15	20	10	9	2	4
900196	C	T	CVD_ALL_CASE	21	30	12	10	10	1	CVD_ALL_CTRL	31	36	26	14	8	9
900200	T	C	CVD_FEM_CASE	20	23	17	6	11	3	CVD_FEM_CTRL	38	58	18	23	12	3
900204	C	G	HELD_FEM_HIRESP	270	430	110	160	110	0	HELD_FEM_LORESP	261	384	138	123	138	0
900205	C	G	HELD_FEM_HIRESP	283	364	202	111	142	30	HELD_FEM_LORESP	274	380	168	138	104	32
900205	C	G	CVD_MAL_CASE	69	90	48	29	32	8	CVD_MAL_CTRL	31	49	13	18	13	0
900223	G	A	HELD_FEM_ADRCASE	43	85	1	42	1	0	HELD_FEM_ADRCTRL	31	57	5	27	3	1

baySNP	A1	A2	COHORT_A	SIZE_A	FQ1_A	FQ2_A	FQ11_A	FQ12_A	FQ22_A	COHORT_B	SIZE_B	FQ1_B	FQ2_B	FQ11_B	FQ12_B	FQ22_B
900225	G	A	HELD_ALL_ADRCASE5ULN	23	0	46	23	0	0	HELD_ALL_ADRCTRL	126	234	18	108	18	0
900225	G	A	HELD_MAL_ADRCASE3ULN	15	0	30	15	0	0	HELD_MAL_ADRCTRL	57	104	10	47	10	0
900227	A	C	HELD_FEM_ADRCASE5ULN	17	33	1	16	1	0	HELD_FEM_ADRCTRL	72	118	26	48	22	2
900233	T	A	HELD_FEM_ADRCASE5ULN	17	23	11	10	3	4	HELD_FEM_ADRCTRL	72	84	60	23	38	11
900236	C	T	HELD_FEM_ADRCASE3ULN	31	50	12	19	12	0	HELD_FEM_ADRCTRL	69	125	13	57	11	1
900236	C	T	HELD_MAL_ADRCASE5ULN	9	18	0	9	0	0	HELD_MAL_ADRCTRL	60	104	16	45	14	1
900241	C	G	HELD_FEM_HIRESP	276	367	185	134	99	43	HELD_FEM_LORESP	275	373	177	124	125	26
900242	G	C	HELD_ALL_ADRCASE5ULN	26	0	52	26	0	0	HELD_ALL_ADRCTRL	132	220	44	99	22	11
900242	G	C	HELD_ALL_ADRCASE3ULN	48	93	3	45	3	0	HELD_ALL_ADRCTRL	132	220	44	99	22	11
900242	G	C	HELD_FEM_ADRCASE5ULN	17	0	34	17	0	0	HELD_FEM_ADRCTRL	72	119	25	49	21	2
900242	G	C	HELD_MAL_ADRCASE3ULN	17	0	34	17	0	0	HELD_MAL_ADRCTRL	60	101	19	50	1	9
900242	G	C	HELD_FEM_ADRCASE	73	136	10	63	10	0	HELD_FEM_ADRCTRL	72	119	25	49	21	2
900242	G	C	HELD_FEM_ADRCASE3ULN	31	59	3	28	3	0	HELD_FEM_ADRCTRL	72	119	25	49	21	2
900242	G	C	HELD_ALL_ADRCASE	136	246	26	113	10	8	HELD_ALL_ADRCTRL	132	220	44	99	22	11
900242	G	C	HELD_MAL_ADRCASE5ULN	9	0	18	9	0	0	HELD_MAL_ADRCTRL	60	101	19	50	1	9

Table 5b p-values of PA SNPs

A SNP is considered as associated to cardiovascular disease, adverse statin response or to efficacy of statin treatment, respectively, when one of the p values is equal or below 0.05.

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
29	HELD_FEM_LIP	0,0996	0,0983	0,0976	0,0441	0,0533	0,0438
29	HELD_ALL_ADR3ULN	0,0483	0,0484	0,0493	0,1053	0,1185	0,1048
29	HELD_ALL_LIP	0,0912	0,0952	0,091	0,0503	0,0625	0,05
52	HELD_ALL_CC	0,0112	0,0128	0,0099	0,0015	0,0023	0,0014
52	HELD_MAL_HDL	0,0237	0,0238	0,0194	0,8213	0,8292	0,8214
52	HELD_FEM_CC	0,0818	0,0956	0,08	0,0293	0,0436	0,0282
52	HELD_MAL_CC	0,1499	0,2053	0,1393	0,0303	0,0547	0,0298
52	HELD_MAL_LIP2	0,1121	0,1133	0,1112	0,0423	0,0429	0,0422
57	HELD_FEM_CC	0,0168	0,008	0,0108	0,0076	0,0106	0,0049
118	HELD_MAL_LIP2	0,1081	0,1089	0,1043	0,0466	0,0501	0,0462
137	HELD_MAL_ADR5ULN	0,0575	0,0872	0,0156	0,0892	0,1027	0,0951
137	HELD_ALL_ADR5ULN	0,0307	0,0274	0,0218	0,2446	0,2504	0,2486
137	HELD_ALL_ADR3ULN	0,034	0,035	0,0255	0,0671	0,0747	0,0686
179	HELD_MAL_ADR5ULN	0,0094	0,0241	0,0154	0,9216	1	0,921
179	HELD_MAL_ADR3ULN	0,0452	0,0479	0,0408	0,5445	0,7636	0,5327
179	HELD_ALL_ADR5ULN	0,0415	0,0537	0,0756	0,7311	0,8135	0,7272
179	HELD_ALL_ADR	0,0691	0,0447	0,0464	0,2487	0,3013	0,2482
240	HELD_ALL_ADR3ULN	0,1154	0,1318	0,0756	0,04	0,0539	0,0281
240	HELD_MAL_ADR3ULN	0,0641	0,0976	0,0399	0,0835	0,1215	0,0507
241	HELD_ALL_ADR3ULN	0,0987	0,0984	0,1033	0,0237	0,0301	0,0262
241	HELD_ALL_ADR5ULN	0,1495	0,1519	0,1611	0,04	0,0527	0,0464
241	HELD_MAL_ADR3ULN	0,1757	0,2127	0,1775	0,0411	0,055	0,0459
288	CVD_ALL	0,1013	0,1098	0,0863	0,0462	0,0557	0,0441
384	CVD_ALL	0,0214	0,022	0,0205	0,1828	0,1946	0,1831
384	HELD_FEM_CC	0,0793	0,0887	0,0704	0,0214	0,0299	0,021
[illegible]	CVD_ALL	0,0955	0,0932	0,0905	0,0387	0,0482	0,0359
542	HELD_FEM_ADR	0,0522	0,0292	0,0417	0,0922	0,1056	0,0907

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
576	HELD_ALL_LIP	0,0349	0,0626	0,0117	0,036	0,0641	0,012
576	HELD_FEM_LIP	0,0403	0,0571	0,0165	0,0416	0,0583	0,017
608	CVD_MAL	0,0031	0,0027	0,002	0,0027	0,0035	0,0035
614	HELD_MAL_HDL	0,0069	0,0113	0,0025	0,0001	0,0001	0
614	HELD_ALL_CC	0,0045	0,0037	0,0031	0,0052	0,008	0,0047
614	HELD_MAL_CC	0,0694	0,1277	0,0689	0,0102	0,0154	0,0101
614	HELD_MAL_LIP	0,1792	0,254	0,1858	0,0113	0,0153	0,0123
614	CVD_ALL	0,1654	0,1652	0,1594	0,0202	0,0237	0,0188
614	HELD_FEM_CC	0,031	0,0198	0,0239	0,0446	0,0537	0,0387
738	CVD_ALL	0,0999	0,1019	0,0962	0,0261	0,0303	0,0257
1056	HELD_ALL_HDL	0,1007	0,1082	0,0989	0,0323	0,0468	0,0304
1056	HELD_FEM_LIP	0,0488	0,0518	0,0403	0,0695	0,09	0,0691
1092	HELD_MAL_ADR5ULN	0,0404	0,0443	0,0114	0,6514	0,7766	0,6465
1524	HELD_MAL_CC2	0,0122	0,0142	0,0107	0,0079	0,0113	0,0062
1524	HELD_ALL_LIP	0,0507	0,0381	0,0237	0,0592	0,0717	0,0581
1524	HELD_ALL_CC	0,0681	0,0671	0,0561	0,025	0,0318	0,0248
1574	CVD_MAL	0,0611	0,0678	0,0422	0,3189	0,4133	0,3254
1582	HELD_MAL_ADR3ULN	0,1522	0,1512	0,0956	0,0468	0,0648	0,0295
1657	HELD_FEM_EFF	0,05	0,0604	0,047	0,4599	0,5588	0,459
1722	CVD_MAL	0,013	0,0128	0,0135	0,3717	0,4376	0,3729
1756	HELD_MAL_ADR5ULN	0,0321	0,0857	0,1003	0,0402	0,063	0,068
1757	HELD_ALL_CC	0,02	0,0205	0,0053	0,3618	0,386	0,3603
1757	HELD_FEM_CC	0,0517	0,0569	0,015	0,1242	0,1342	0,1193
1757	HELD_FEM_VEFF	0,1217	0,1247	0,1208	0,0423	0,0505	0,0422
1757	HELD_MAL_ADR	0,0536	0,05	0,0501	0,6703	0,7693	0,6702
1765	HELD_ALL_LIP	0,0466	0,0494	0,0442	0,3068	0,3533	0,3058
1767	HELD_ALL_ADR3ULN	0,0082	0,0075	0,0036	0,0053	0,0066	0,0026
1767	HELD_ALL_ADR5ULN	0,0608	0,0467	0,0302	0,0196	0,0231	0,0086
1767	HELD_MAL_ADR5ULN	0,183	0,216	0,0679	0,075	0,1229	0,0194
1767	HELD_FEM_ADR3ULN	0,0371	0,0348	0,0221	0,0341	0,0408	0,0251
1767	HELD_MAL_ADR3ULN	0,1692	0,1875	0,1061	0,0606	0,0741	0,0334
1837	HELD_ALL_ADR3ULN	0,0408	0,0398	0,0402	0,0225	0,0282	0,0196

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
1837	HELD_FEM_LIP	0,0337	0,0356	0,0328	0,3132	0,3242	0,3131
1837	HELD_ALL_LIP	0,0466	0,046	0,0452	0,3884	0,3987	0,3879
1837	HELD_ALL_ADR	0,052	0,0488	0,0514	0,0709	0,075	0,0708
1854	HELD_FEM_LIP	0,0512	0,0527	0,05	0,0661	0,07	0,0658
1862	HELD_FEM_LIP	0,0562	0,058	0,0534	0,0231	0,0264	0,0229
2085	HELD_FEM_CC	0,0149	0,0109	0,0118	0,0081	0,0096	0,0081
2085	HELD_ALL_CC	0,0388	0,038	0,0345	0,0185	0,02	0,0183
2093	HELD_MAL_CC	0,047	0,0249	0,037	0,0015	0,002	0,0013
2093	HELD_ALL_CC	0,1596	0,1532	0,1414	0,04	0,0501	0,0383
2109	HELD_MAL_HDL	0,0044	0,0028	0,0023	0,0341	0,0543	0,0299
2109	HELD_ALL_HDL	0,0187	0,0127	0,0131	0,059	0,065	0,0546
2109	HELD_ALL_LIP2	0,0438	0,0439	0,0434	0,015	0,0152	0,0148
2109	HELD_FEM_LIP	0,0612	0,0563	0,059	0,0214	0,0277	0,0209
2124	HELD_MAL_LIP	0,1532	0,2284	0,153	0,0434	0,0557	0,0433
2140	HELD_FEM_UEFF	0,0437	0,0427	0,0203	0,009	0,0116	0,0069
2140	HELD_FEM_EFF	0,0174	0,0167	0,0136	0,0082	0,009	0,008
2140	HELD_MAL_ADR	0,0596	0,0738	0,0227	0,0301	0,0429	0,0285
2140	HELD_FEM_VEFF	0,0915	0,0872	0,0888	0,0284	0,0379	0,0277
2141	HELD_MAL_ADR3ULN	0,0844	0,0968	0,0461	0,0218	0,0238	0,0116
2141	HELD_FEM_UEFF	0,0776	0,0859	0,0221	0,1372	0,1469	0,1323
2141	HELD_MAL_ADR	0,0548	0,0515	0,0254	0,0347	0,0399	0,0344
2186	HELD_MAL_ADR5ULN	0,0287	0,0843	0,1009	0,0498	0,0718	0,0798
2187	HELD_FEM_ADR3ULN	0,0517	0,0567	0,0507	0,0495	0,0613	0,0529
2192	HELD_FEM_ADR	0,0008	0,0011	0,0003	0,0011	0,0014	0,0004
2192	HELD_FEM_ADR3ULN	0,0114	0,0187	0,0015	0,0146	0,0232	0,0019
2192	HELD_ALL_ADR	0,0234	0,0113	0,0173	0,0053	0,0068	0,0044
2192	HELD_FEM_ADR5ULN	0,0613	0,1149	0,0155	0,073	0,1305	0,0181
2192	HELD_ALL_ADR3ULN	0,1807	0,1865	0,1212	0,0607	0,0756	0,039
2203	HELD_FEM_LIP	0,0132	0,011	0,0126	0,0101	0,0118	0,0098
2203	HELD_ALL_LIP	0,0296	0,0294	0,029	0,042	0,0442	0,0422
2217	HELD_MAL_CC	0,0089	0,0048	0,0053	0,0074	0,0101	0,0071
2217	CVD_FEM	0,1624	0,1741	0,1076	0,0384	0,0539	0,0314

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
2281	HELD_FEM_CC	0,0422	0,0439	0,0393	0,0076	0,0102	0,0072
2281	HELD_MAL_CC	0,0529	0,0593	0,0174	0,0834	0,1238	0,0807
2284	HELD_MAL_LIP	0,0754	0,0848	0,0464	0,0227	0,0292	0,0137
2290	HELD_MAL_CC	0,0301	0,0636	0,0267	0,0022	0,0031	0,0017
2327	HELD_MAL_ADR	0,0279	0,0298	0,0262	0,0923	0,1092	0,092
2327	HELD_MAL_ADR5ULN	0,047	0,0358	0,0381	0,3085	0,4458	0,3068
2327	HELD_MAL_ADR3ULN	0,0396	0,0397	0,0429	0,0919	0,116	0,0897
2327	HELD_FEM_EFF	0,0462	0,0457	0,0458	0,0998	0,1039	0,0998
2353	CVD_MAL	0,0703	0,0407	0,0139	0,0223	0,0233	0,0031
2353	HELD_ALL_CC	0,0255	0,0122	0,0224	0,0659	0,0929	0,0654
2353	CVD_ALL	0,1352	0,1146	0,0973	0,0468	0,0506	0,0347
2353	HELD_FEM_CC	0,0743	0,0491	0,0628	0,1836	0,3092	0,1885
2371	HELD_ALL_LIP2	0,018	0,018	0,0181	0,043	0,0444	0,0432
2376	HELD_ALL_LIP2	0,03	0,038	0,0302	0,0327	0,0411	0,0329
2401	HELD_FEM_UEFF	0,0263	0,0256	0,0266	0,1128	0,1233	0,1146
2463	HELD_ALL_CC	0,0122	0,0147	0,0028	0,0144	0,0168	0,0033
2463	HELD_FEM_CC	0,0257	0,0328	0,0074	0,0307	0,0376	0,0088
2463	HELD_FEM_LIP2	0,0915	0,0988	0,0431	0,7177	0,7419	0,718
2755	HELD_FEM_ADR	0,0203	0,0192	0,0178	0,0222	0,024	0,022
2755	HELD_ALL_ADR	0,0325	0,035	0,03	0,0499	0,0513	0,0496
2755	HELD_FEM_EFF	0,0455	0,0449	0,0446	0,4065	0,4262	0,4065
2925	HELD_FEM_VEFF	0,0168	0,0169	0,0162	0,0055	0,0058	0,0055
2925	HELD_FEM_UEFF	0,0184	0,0176	0,0181	0,009	0,0119	0,0088
3043	HELD_FEM_ADR3ULN	0,031	0,0498	0,0233	0,0515	0,0764	0,0376
3152	HELD_FEM_VEFF	0,0204	0,0206	0,0196	0,3254	0,333	0,3253
3214	HELD_FEM_VEFF	0,0379	0,0331	0,0261	0,4369	0,4475	0,437
3215	HELD_MAL_ADR5ULN	0,0093	0,1304	0,041	0,0096	0,1304	0,0423
3237	HELD_FEM_CC	0,0174	0,0276	0,0167	0,0218	0,0323	0,0211
3241	HELD_MAL_ADR	0,111	0,1115	0,1048	0,0334	0,0418	0,033
3826	HELD_MAL_ADR5ULN	0,2155	0,1993	0,0862	0,0716	0,1186	0,0187
3826	HELD_ALL_ADR5ULN	0,254	0,2956	0,1522	0,0707	0,0873	0,038
3826	HELD_MAL_ADR3ULN	0,2528	0,2755	0,1635	0,0732	0,1143	0,044

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
3842	CVD_ALL	0,0096	0,0142	0,0014	0,0108	0,0157	0,0016
3842	CVD_MAL	0,0682	0,0966	0,0207	0,0735	0,1027	0,0222
3842	CVD_FEM	0,0717	0,1136	0,0359	0,0751	0,1165	0,0376
3843	HELD_MAL_CC2	0,0207	0,0236	0,0084	0,0758	0,1046	0,0759
3843	HELD_FEM_HDL	0,0447	0,024	0,0146	0,1239	0,1687	0,1233
3869	HELD_FEM_UEFF	0,0491	0,0538	0,0488	0,0211	0,0244	0,0202
3942	HELD_FEM_UEFF	0,0206	0,0152	0,0122	0,0028	0,0041	0,0029
4018	HELD_MAL_LIP	0,1128	0,1214	0,0532	0,037	0,0451	0,0313
4206	HELD_ALL_ADR3ULN	0,1055	0,1128	0,1103	0,041	0,0532	0,0418
4206	HELD_FEM_ADR	0,1218	0,1204	0,1193	0,0436	0,0574	0,0434
4206	HELD_ALL_ADR5ULN	0,1204	0,1214	0,1254	0,0472	0,0639	0,0488
4527	CVD_ALL	0,0044	0,0031	0,0012	0,2436	0,2844	0,2451
4527	HELD_FEM_LIP2	0,0441	0,0429	0,0424	0,0147	0,0157	0,0145
4527	HELD_MAL_CC	0,0814	0,0496	0,0661	0,0208	0,0296	0,0197
4527	HELD_MAL_CC2	0,0599	0,0604	0,0583	0,0256	0,0378	0,0267
4527	HELD_ALL_ADR3ULN	0,0688	0,0608	0,0728	0,0316	0,0402	0,0354
4527	HELD_ALL_CC2	0,1329	0,1396	0,1355	0,0449	0,048	0,0461
4527	HELD_ALL_ADR5ULN	0,0796	0,0668	0,1142	0,0478	0,0592	0,0569
4544	HELD_MAL_ADR3ULN	0,0116	0,0154	0,0146	0,0043	0,0062	0,0063
4544	HELD_MAL_ADR	0,0731	0,0643	0,0601	0,0283	0,0348	0,0274
4544	HELD_ALL_ADR	0,086	0,0869	0,0832	0,0279	0,0308	0,0276
4544	HELD_ALL_ADR3ULN	0,1284	0,1257	0,1312	0,0497	0,054	0,0537
4545	HELD_MAL_ADR3ULN	0,0116	0,0154	0,0146	0,0043	0,0062	0,0063
4545	HELD_MAL_ADR	0,0629	0,0569	0,0516	0,0234	0,0247	0,0226
4545	HELD_ALL_ADR	0,0947	0,0982	0,0917	0,0318	0,0385	0,0314
4668	HELD_ALL_ADR5ULN	0,0773	0,0782	0,0348	0,1143	0,1279	0,1111
4669	HELD_FEM_EFF	0,1061	0,1031	0,1053	0,0415	0,0458	0,0412
4718	HELD_MAL_LIP	0,0234	0,0261	0,006	0,2267	0,2838	0,2221
4818	HELD_MAL_LIP	0,0117	0,0073	0,0072	0,0904	0,1138	0,0946
4827	HELD_MAL_ADR5ULN	0,0267	0,0922	0,0873	0,6447	0,708	0,6539
4838	HELD_ALL_CC2	0,1354	0,1425	0,1366	0,047	0,0495	0,0469
4856	CVD_MAL	0,0123	0,0338	0,0089	0,0129	0,0349	0,0094

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
4868	HELD_MAL_ADR	0,0492	0,055	0,0155	0,2125	0,24	0,2117
4868	HELD_MAL_ADR5ULN	0,0236	0,1201	0,1125	0,412	0,5267	0,4261
4887	HELD_MAL_CC	0,0119	0,0064	0,0075	0,0066	0,0077	0,0042
4887	HELD_ALL_CC	0,0826	0,0705	0,0811	0,0378	0,0429	0,0378
4912	HELD_MAL_LIP	0,2542	0,3163	0,2499	0,0325	0,053	0,0303
4951	HELD_ALL_ADR3ULN	0,0019	0,0018	0,0018	0,5543	0,6301	0,5547
4951	HELD_FEM_ADR3ULN	0,0028	0,0029	0,003	0,237	0,284	0,2372
4951	HELD_FEM_ADR5ULN	0,0049	0,0039	0,0088	0,0663	0,0845	0,0657
4951	HELD_ALL_ADR5ULN	0,006	0,0054	0,0103	0,0586	0,0675	0,0589
4951	HELD_FEM_ADR	0,0104	0,0096	0,0091	0,1202	0,1247	0,12
4951	HELD_ALL_ADR	0,0233	0,0229	0,022	0,1271	0,1376	0,1269
4952	HELD_ALL_ADR3ULN	0,0018	0,0017	0,0015	0,6771	0,7182	0,6774
4952	HELD_FEM_ADR3ULN	0,0019	0,0017	0,002	0,2491	0,2848	0,2496
4952	HELD_FEM_ADR5ULN	0,0029	0,0023	0,0048	0,0938	0,1245	0,094
4952	HELD_ALL_ADR5ULN	0,0062	0,0056	0,009	0,1013	0,1264	0,102
4966	HELD_MAL_LIP	0,0276	0,027	0,0099	0,0138	0,0207	0,0122
4966	HELD_MAL_ADR	0,0409	0,046	0,0375	0,0937	0,1211	0,0933
4966	HELD_FEM_CC	0,0951	0,1056	0,0936	0,0442	0,0696	0,0434
5019	CVD_FEM	0,0011	0,001	0,0007	0,0055	0,0087	0,0053
5019	HELD_ALL_CC2	0,0043	0,0045	0,0043	0,0479	0,0599	0,0477
5019	HELD_MAL_HDL	0,0666	0,0705	0,0594	0,0076	0,0117	0,0068
5019	HELD_ALL_LIP	0,0362	0,0383	0,0342	0,0109	0,0125	0,0108
5019	HELD_MAL_CC2	0,0182	0,0179	0,0186	0,0143	0,0167	0,0138
5165	HELD_FEM_ADR3ULN	0,0193	0,0172	0,0174	0,064	0,0907	0,0714
5165	HELD_MAL_ADR5ULN	0,0267	0,0922	0,0873	0,6447	0,708	0,6539
5165	HELD_FEM_ADR	0,0405	0,0271	0,0268	0,2071	0,2511	0,2059
5165	HELD_FEM_ADR5ULN	0,0414	0,0557	0,0471	0,0836	0,1012	0,101
5278	HELD_MAL_ADR5ULN	0,0556	0,0596	0,1196	0,046	0,0769	0,0577
5287	HELD_FEM_VEFF	0,0487	0,0497	0,0438	0,0093	0,0101	0,0088
5320	CVD_FEM	0,0342	0,0343	0,0283	0,0279	0,0303	0,0274
5324	HELD_FEM_VEFF	0,0912	0,0915	0,0898	0,0318	0,0391	0,0317
5373	HELD_FEM_ADR5ULN	0,0095	0,0124	0,0056	0,0061	0,0088	0,0028

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
5373	HELD_ALL_ADR5ULN	0,0776	0,0691	0,0342	0,0287	0,0398	0,0217
5375	HELD_FEM_ADR5ULN	0,0092	0,0136	0,0056	0,0058	0,0081	0,0027
5375	HELD_ALL_ADR5ULN	0,138	0,1305	0,0564	0,0585	0,0615	0,0495
5376	HELD_MAL_ADR5ULN	0,0067	0,1212	0,0373	0,0069	0,1212	0,0386
5377	HELD_FEM_ADR	0,0201	0,019	0,019	0,2353	0,2692	0,2345
5377	HELD_FEM_ADR5ULN	0,0497	0,0546	0,0353	0,0289	0,044	0,0203
5517	HELD_MAL_ADR	0,0831	0,1183	0,0317	0,4341	0,6834	0,4294
5518	HELD_FEM_ADR5ULN	0,0341	0,1839	0,0637	0,0346	0,1839	0,0647
5564	CVD_MAL	0,0139	0,0146	0,0159	0,1077	0,1348	0,1057
5569	HELD_MAL_ADR5ULN	0,1012	0,1304	0,0676	0,0445	0,0667	0,0238
5569	HELD_ALL_ADR5ULN	0,1458	0,1504	0,0609	0,0502	0,0672	0,04
5716	HELD_ALL_ADR3ULN	0,0067	0,0064	0,0069	0,0024	0,0025	0,0023
5716	HELD_FEM_ADR3ULN	0,0071	0,0063	0,0059	0,0027	0,0037	0,0024
5716	HELD_ALL_ADR5ULN	0,0248	0,0232	0,0218	0,0092	0,0124	0,0092
5716	HELD_FEM_ADR5ULN	0,0769	0,0784	0,0685	0,0334	0,0412	0,0321
5717	HELD_ALL_ADR5ULN	0,1212	0,1272	0,097	0,0433	0,049	0,0427
5717	CVD_FEM	0,0496	0,0575	0,0431	0,0551	0,0634	0,054
5850	HELD_MAL_CC	0,0304	0,0344	0,0113	0,1197	0,1794	0,1186
5959	CVD_MAL	0,064	0,0647	0,0552	0,0467	0,0678	0,048
6151	HELD_MAL_ADR	0,0502	0,0501	0,0488	0,3223	0,3964	0,3221
6236	HELD_ALL_ADR	0,0472	0,051	0,0424	0,0867	0,0953	0,0864
6277	HELD_FEM_ADR5ULN	0,0014	0,0053	0,0049	0,0127	0,0215	0,0185
6277	HELD_ALL_ADR5ULN	0,0041	0,0135	0,026	0,0832	0,1012	0,0964
6277	HELD_FEM_ADR	0,0251	0,0239	0,0079	0,0157	0,0186	0,0149
6277	HELD_FEM_ADR3ULN	0,0147	0,0126	0,0119	0,0167	0,02	0,0196
6313	HELD_FEM_UEFF	0,0369	0,0357	0,0376	0,1201	0,1519	0,1204
6369	HELD_FEM_LIP	0,1311	0,145	0,1269	0,0461	0,0594	0,0457
6374	HELD_ALL_ADR3ULN	0,0338	0,0325	0,0352	0,0091	0,0107	0,0099
6374	HELD_MAL_ADR3ULN	0,0498	0,0564	0,044	0,011	0,0152	0,0121
6396	HELD_MAL_CC	0,0165	0,0238	0,0048	0,0233	0,031	0,0066
6396	HELD_ALL_CC	0,0528	0,0316	0,0496	0,0334	0,0403	0,0323
6396	CVD_FEM	0,1144	0,0874	0,0928	0,046	0,0631	0,0442

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
6396	CVD_ALL	0,1388	0,1213	0,0933	0,0516	0,0541	0,0465
6486	HELD_ALL_CC2	0,1446	0,1479	0,1283	0,0373	0,0528	0,0345
6520	HELD_MAL_ADR5ULN	0,0003	0,0081	0,0068	0,1889	0,3068	0,2137
6520	HELD_MAL_ADR3ULN	0,0021	0,005	0,0051	0,1797	0,2122	0,1939
6520	HELD_ALL_ADR5ULN	0,022	0,0339	0,0666	0,0816	0,0892	0,093
6520	HELD_MAL_ADR	0,0743	0,0876	0,0283	0,322	0,3417	0,3212
6522	HELD_FEM_ADR3ULN	0,0618	0,0604	0,0447	0,2761	0,3091	0,284
6522	HELD_FEM_ADR	0,0523	0,0465	0,0502	0,0894	0,0983	0,0882
6524	HELD_MAL_ADR3ULN	0,0215	0,0213	0,0096	0,0128	0,0173	0,0106
6596	HELD_FEM_ADR3ULN	0	0	0	0	0,0001	0
6596	HELD_FEM_ADR5ULN	0,0001	0,0006	0,0004	0,0001	0,0011	0,0008
6596	HELD_ALL_ADR3ULN	0,0003	0,0006	0,0005	0,0005	0,001	0,001
6596	HELD_FEM_ADR	0,0008	0,0011	0,0005	0,0014	0,0018	0,0009
6596	HELD_ALL_ADR5ULN	0,0025	0,0064	0,0064	0,0036	0,0085	0,0094
6596	HELD_ALL_ADR	0,0199	0,0229	0,0186	0,0253	0,0286	0,0236
6734	HELD_ALL_CC	0,04	0,0752	0,0208	0,0463	0,0816	0,0241
6743	HELD_ALL_ADR	0,0299	0,0298	0,0293	0,5743	0,6388	0,5742
7128	HELD_ALL_ADR3ULN	0,0099	0,0103	0,0081	0,0032	0,0042	0,0021
7128	HELD_FEM_ADR3ULN	0,0161	0,014	0,0134	0,011	0,0121	0,0085
7128	HELD_ALL_ADR5ULN	0,0787	0,0793	0,0702	0,029	0,0316	0,0217
7128	HELD_FEM_ADR	0,0447	0,0497	0,0437	0,0497	0,0519	0,0496
7128	HELD_FEM_ADR5ULN	0,0996	0,1085	0,0925	0,0561	0,0763	0,0458
7363	HELD_FEM_LIP	0,0763	0,0816	0,0701	0,0282	0,0385	0,0276
7363	HELD_ALL_LIP	0,0741	0,0762	0,0712	0,0298	0,0314	0,0299
7409	HELD_FEM_ADR5ULN	0,0051	0,0049	0,01	0,0025	0,0051	0,0054
7409	HELD_FEM_ADR3ULN	0,0303	0,0175	0,0316	0,0135	0,0165	0,0172
7409	HELD_MAL_ADR5ULN	0,1823	0,1987	0,0669	0,0691	0,128	0,017
8138	HELD_MAL_LIP	0,0177	0,0193	0,0183	0,0079	0,0088	0,0069
8138	HELD_MAL_CC	0,0107	0,011	0,0077	0,4323	0,4651	0,4318
8138	HELD_ALL_LIP	0,0401	0,039	0,0399	0,0761	0,0923	0,0757
8168	HELD_MAL_LIP	0,0229	0,0222	0,026	0,011	0,0203	0,0132
8168	HELD_FEM_LIP	0,0241	0,0204	0,0226	0,1027	0,1374	0,1017

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
8210	HELD_ALL_ADR3ULN	0,0096	0,0098	0,0098	0,7816	0,8049	0,7818
8210	HELD_FEM_ADR3ULN	0,0141	0,0135	0,0159	0,4056	0,4314	0,4063
8210	HELD_FEM_ADR	0,0222	0,0225	0,0198	0,2153	0,2257	0,2151
8210	HELD_ALL_ADR	0,0215	0,021	0,0203	0,2277	0,2424	0,2276
8241	HELD_FEM_LIP	0,0187	0,0132	0,0085	0,0063	0,0082	0,0058
8241	HELD_ALL_LIP	0,159	0,1538	0,1542	0,0425	0,0474	0,0407
8249	HELD_ALL_ADR3ULN	0,0387	0,0449	0,0478	0,0458	0,0517	0,0569
8249	HELD_ALL_ADR5ULN	0,0455	0,0847	0,0653	0,0527	0,0943	0,0765
8480	CVD_FEM	0,0462	0,0244	0,0232	0,0026	0,0039	0,0008
8480	CVD_MAL	0,1317	0,1542	0,0466	0,0145	0,0286	0,0026
8577	HELD_ALL_ADR3ULN	0,067	0,0657	0,0615	0,0252	0,0333	0,0264
8577	HELD_ALL_ADR	0,0786	0,0752	0,0779	0,0341	0,0374	0,0339
8577	HELD_ALL_ADR5ULN	0,1543	0,1417	0,1606	0,05	0,0577	0,0532
8578	HELD_ALL_ADR3ULN	0,0857	0,0895	0,0777	0,0407	0,0491	0,0421
8653	HELD_MAL_ADR	0,0015	0,002	0,0012	0,004	0,005	0,0032
8653	HELD_MAL_ADR3ULN	0,0104	0,0118	0,0049	0,0239	0,0259	0,0099
8653	HELD_MAL_ADR5ULN	0,0243	0,0358	0,0061	0,0499	0,0688	0,0107
8653	HELD_ALL_ADR3ULN	0,0509	0,0714	0,04	0,0799	0,1109	0,0679
8816	HELD_FEM_LIP2	0,0115	0,0116	0,0106	0,0057	0,0067	0,0056
8816	HELD_FEM_HDL	0,0254	0,0258	0,0184	0,0126	0,0148	0,0119
8816	HELD_ALL_CC2	0,0198	0,0205	0,0188	0,0352	0,0373	0,0354
8816	CVD_ALL	0,0862	0,084	0,0801	0,0253	0,0334	0,0231
8816	HELD_FEM_CC2	0,0732	0,0788	0,0699	0,0263	0,0349	0,0263
8816	HELD_MAL_HDL	0,0827	0,0805	0,0459	0,9552	1	0,9552
8931	HELD_FEM_ADR3ULN	0,0638	0,0558	0,0365	0,1009	0,1129	0,0851
8943	HELD_MAL_ADR3ULN	0,115	0,1264	0,0702	0,0366	0,0409	0,0217
9243	HELD_FEM_VEFF	0,0407	0,0439	0,0252	0,155	0,1691	0,1544
9243	HELD_MAL_ADR5ULN	0,1035	0,0777	0,0285	0,2159	0,2497	0,1855
9243	HELD_FEM_UEFF	0,1004	0,12	0,0335	0,1733	0,2118	0,1696
9523	HELD_MAL_ADR5ULN	0,0425	0,0646	0,0613	0,0575	0,0785	0,0889
9940	HELD_MAL_CC	0,0213	0,0425	0,0073	0,0294	0,0542	0,0099
9940	HELD_ALL_CC	0,0341	0,0266	0,0312	0,0231	0,0354	0,0225

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
10091	HELD_ALL_ADR3ULN	0,0852	0,0819	0,1028	0,0428	0,0524	0,0487
10541	HELD_FEM_UEFF	0,0349	0,0191	0,0267	0,0305	0,0477	0,0256
10541	HELD_FEM_VEFF	0,066	0,0484	0,0643	0,0206	0,0217	0,02
10600	CVD_MAL	0,0475	0,0359	0,0348	0,0046	0,0121	0,0029
10600	HELD_ALL_HDL	0,0207	0,0298	0,0058	0,0231	0,0325	0,0064
10600	HELD_MAL_HDL	0,056	0,1137	0,0231	0,0625	0,1228	0,0256
10745	HELD_MAL_LIP	0,0926	0,0862	0,085	0,056	0,0701	0,0491
10748	HELD_MAL_LIP	0,1405	0,1855	0,1371	0,05	0,0676	0,0547
10749	HELD_FEM_LIP	0,0593	0,0591	0,055	0,0232	0,026	0,023
10785	CVD_MAL	0,1111	0,1415	0,1247	0,0383	0,0491	0,0448
10811	HELD_FEM_LIP2	0,0827	0,0859	0,0821	0,0442	0,0465	0,0435
10811	CVD_ALL	0,1149	0,1091	0,1111	0,0524	0,0646	0,0498
10830	HELD_ALL_LIP2	0,0065	0,0065	0,0062	0,0036	0,0039	0,0036
10830	HELD_ALL_LIP	0,0187	0,0191	0,018	0,0037	0,0048	0,0037
10830	HELD_MAL_LIP2	0,0389	0,0395	0,0383	0,011	0,0112	0,0109
10830	CVD_FEM	0,0268	0,0239	0,0238	0,0125	0,0141	0,0121
10830	HELD_MAL_LIP	0,0742	0,0873	0,0613	0,0224	0,0279	0,0219
10830	HELD_FEM_LIP	0,1364	0,1403	0,134	0,0428	0,0556	0,0426
10949	HELD_FEM_VEFF	0,0543	0,0577	0,0536	0,0352	0,0374	0,0351
10949	HELD_FEM_EFF	0,0748	0,0744	0,0743	0,0356	0,04	0,0356
10962	CVD_FEM	0,0113	0,0275	0,0091	0,0218	0,0457	0,0177
10962	HELD_ALL_ADR3ULN	0,1473	0,1615	0,043	0,2642	0,3199	0,258
10966	HELD_ALL_ADR3ULN	0,1289	0,1277	0,0351	0,1511	0,1736	0,1447
10966	HELD_ALL_ADR5ULN	0,1509	0,1612	0,0683	0,0587	0,0794	0,0483
11000	HELD_MAL_LIP2	0,0379	0,0378	0,0375	0,0125	0,0143	0,0123
11000	CVD_FEM	0,0202	0,0198	0,0161	0,9584	1	0,9584
11000	HELD_MAL_ADR3ULN	0,0414	0,0384	0,0554	0,0307	0,0378	0,0344
11000	HELD_ALL_LIP2	0,0965	0,0965	0,096	0,0351	0,0358	0,0348
11000	HELD_MAL_ADR5ULN	0,0477	0,0555	0,0971	0,053	0,0607	0,0618
11001	HELD_MAL_LIP2	0,03	0,0288	0,0297	0,0103	0,0111	0,0102
11001	HELD_ALL_LIP2	0,0662	0,0652	0,0658	0,0235	0,0241	0,0232
11001	CVD_FEM	0,0325	0,0293	0,0266	0,9749	1	0,9749

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
11001	HELD_MAL_ADR3ULN	0,0414	0,0384	0,0554	0,0307	0,0378	0,0344
11001	HELD_ALL_LIP	0,1116	0,1195	0,1013	0,0482	0,057	0,0473
11020	HELD_MAL_ADR3ULN	0,1685	0,1457	0,087	0,0596	0,0761	0,049
11073	HELD_FEM_LIP	0,111	0,1116	0,1085	0,0331	0,0361	0,0328
11073	HELD_ALL_CC2	0,096	0,0963	0,0954	0,0453	0,0475	0,0437
11192	HELD_FEM_ADR5ULN	0,0153	0,0191	0,0329	0,2812	0,2901	0,2893
11192	HELD_FEM_ADR3ULN	0,0257	0,0216	0,0353	0,2446	0,3079	0,249
11248	HELD_FEM_ADR3ULN	0,0183	0,0153	0,0137	0,025	0,0322	0,0203
11248	HELD_ALL_ADR	0,1078	0,1144	0,1071	0,042	0,0434	0,0419
11410	HELD_FEM_VEFF	0,0091	0,0089	0,0085	0,088	0,0909	0,0879
11448	HELD_MAL_HDL	0,0019	0,0012	0,0015	0,0002	0,0003	0,0002
11448	HELD_MAL_LIP	0,0055	0,0027	0,0061	0,0034	0,005	0,0042
11448	HELD_MAL_LIP2	0,0059	0,0056	0,0058	0,0233	0,0245	0,0234
11448	HELD_ALL_LIP2	0,0108	0,0106	0,0109	0,0119	0,0124	0,012
11448	HELD_ALL_HDL	0,0647	0,0708	0,0648	0,0138	0,0215	0,0142
11448	HELD_FEM_ADR	0,0637	0,0601	0,0603	0,0162	0,0199	0,0156
11448	HELD_ALL_ADR	0,0576	0,0568	0,055	0,017	0,0209	0,0166
11448	HELD_ALL_CC	0,0976	0,1314	0,0453	0,0671	0,0727	0,0652
11450	HELD_MAL_LIP	0,0068	0,0052	0,0066	0,0007	0,0012	0,0009
11456	CVD_FEM	0,0026	0,0043	0,0016	0,0038	0,0058	0,0023
11462	HELD_MAL_LIP2	0,0302	0,0225	0,0284	0,0091	0,0109	0,0091
11462	HELD_ALL_LIP2	0,0406	0,0368	0,0362	0,0384	0,0431	0,0387
11483	HELD_FEM_ADR5ULN	0,032	0,0455	0,0589	0,0562	0,0771	0,0832
11483	HELD_FEM_ADR3ULN	0,0442	0,034	0,0495	0,0824	0,0989	0,0958
11483	HELD_FEM_ADR	0,0628	0,0468	0,045	0,1531	0,2	0,1477
11531	HELD_FEM_CC	0,1229	0,1273	0,0498	0,0189	0,0335	0,0137
11536	HELD_ALL_CC	0,0789	0,085	0,0365	0,7564	0,8525	0,7562
11537	HELD_MAL_ADR	0,1696	0,1625	0,1616	0,0467	0,0604	0,0455
11558	HELD_MAL_LIP2	0,0028	0,0023	0,0028	0,0058	0,0064	0,0058
11558	HELD_ALL_LIP2	0,011	0,0105	0,011	0,005	0,0054	0,005
11558	HELD_ALL_CC	0,0533	0,0503	0,05	0,102	0,1242	0,1013
11585	HELD_MAL_CC	0,0414	0,0372	0,0136	0,0108	0,0193	0,0094

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
11594	HELD_ALL_ADR3ULN	0,0819	0,0998	0,035	0,0195	0,0196	0,0069
11594	HELD_MAL_ADR	0,0312	0,0403	0,0277	0,0365	0,0462	0,0324
11614	HELD_FEM_CC	0,0473	0,0577	0,0234	0,0572	0,0644	0,0587
11614	HELD_MAL_CC2	0,052	0,0518	0,0331	0,0346	0,0482	0,0373
11614	HELD_ALL_CC	0,0923	0,1151	0,0429	0,25	0,2653	0,2502
11614	HELD_ALL_HDL	0,0563	0,0558	0,0499	0,9149	1	0,9149
11631	HELD_MAL_ADR5ULN	0,0386	0,0478	0,0304	0,0117	0,0156	0,0155
11631	HELD_MAL_ADR3ULN	0,1371	0,1283	0,1422	0,046	0,0572	0,051
11637	HELD_FEM_LIP	0,0168	0,0155	0,0113	0,0321	0,0343	0,0317
11637	HELD_ALL_LIP	0,0303	0,0314	0,0288	0,0148	0,0186	0,0149
11637	CVD_MAL	0,0697	0,0701	0,0767	0,0248	0,0373	0,0272
11637	CVD_ALL	0,0723	0,0759	0,073	0,0254	0,0318	0,0262
11641	HELD_MAL_ADR	0,0142	0,0141	0,0129	0,126	0,1468	0,1257
11645	HELD_FEM_CC	0,0369	0,0544	0,0366	0,0456	0,0639	0,0454
11646	HELD_FEM_LIP	0,0865	0,0938	0,0854	0,0359	0,0387	0,0356
11646	HELD_ALL_LIP	0,0788	0,077	0,078	0,0438	0,0453	0,0431
11652	HELD_MAL_LIP	0,0422	0,0402	0,0403	0,9398	1	0,9398
11727	HELD_ALL_ADR5ULN	0,0133	0,0169	0,001	0,0033	0,0029	0,0001
11727	HELD_MAL_ADR3ULN	0,0139	0,0156	0,0019	0,0035	0,0042	0,0002
11727	HELD_MAL_ADR5ULN	0,0632	0,0556	0,0165	0,0205	0,0202	0,003
11727	HELD_ALL_ADR3ULN	0,0384	0,0373	0,0163	0,0076	0,0071	0,0036
11727	HELD_FEM_ADR5ULN	0,1918	0,2611	0,0649	0,0728	0,128	0,0182
11728	HELD_ALL_ADR5ULN	0,1462	0,1458	0,095	0,0556	0,0654	0,0388
11914	HELD_MAL_ADR3ULN	0,2466	0,3289	0,2216	0,0257	0,0387	0,0248
11938	HELD_ALL_ADR3ULN	0,0089	0,0095	0,0046	0,392	0,459	0,3897
11938	HELD_ALL_ADR5ULN	0,0169	0,0157	0,0114	0,8154	0,8766	0,815
11938	HELD_FEM_ADR3ULN	0,0449	0,0479	0,0352	0,6253	0,6469	0,6247
11950	HELD_MAL_ADR5ULN	0,0201	0,0516	0,0044	0,0125	0,0113	0,0014
11950	HELD_MAL_ADR3ULN	0,0154	0,0166	0,0066	0,0323	0,0548	0,0214
11950	HELD_MAL_ADR	0,0516	0,0613	0,0496	0,3586	0,4444	0,3582
11951	HELD_MAL_ADR5ULN	0,0424	0,0545	0,0114	0,0236	0,0423	0,0037
11951	HELD_FEM_UEFF	0,0259	0,0235	0,0107	0,0733	0,0868	0,0749

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
12008	HELD_ALL_ADR	0,0485	0,062	0,0449	0,0524	0,0663	0,0486
12031	HELD_ALL_ADR3ULN	0,0028	0,0024	0,0026	0,63	0,7148	0,6303
12031	HELD_FEM_ADR5ULN	0,0046	0,0039	0,0086	0,0566	0,0838	0,0562
12031	HELD_ALL_ADR5ULN	0,0047	0,0041	0,0086	0,0504	0,0658	0,0508
12031	HELD_FEM_ADR3ULN	0,0056	0,0063	0,006	0,2925	0,3532	0,2929
12031	HELD_ALL_ADR	0,0138	0,0141	0,0129	0,1033	0,113	0,1031
12031	HELD_FEM_ADR	0,0147	0,0143	0,0131	0,1206	0,1247	0,1203
12032	HELD_FEM_UEFF	0,0304	0,0139	0,0261	0,0076	0,0093	0,0078
12032	HELD_FEM_ADR	0,1261	0,1063	0,0841	0,0343	0,0448	0,031
12032	HELD_ALL_ADR	0,0928	0,0748	0,0517	0,0359	0,0376	0,0341
12032	HELD_FEM_VEFF	0,0639	0,0469	0,0614	0,0748	0,0929	0,0737
12148	HELD_MAL_ADR5ULN	0,0166	0,0158	0,026	0,0087	0,0155	0,0126
12148	HELD_MAL_ADR	0,0376	0,0431	0,0328	0,0142	0,0207	0,0139
12148	HELD_MAL_ADR3ULN	0,0616	0,0647	0,085	0,0349	0,046	0,0398
12207	HELD_MAL_ADR5ULN	0,0034	0,0036	0,002	0,6147	0,7792	0,6195
12207	HELD_MAL_ADR	0,003	0,0028	0,002	0,1131	0,1259	0,1125
12207	HELD_MAL_ADR3ULN	0,024	0,0181	0,0298	0,5888	0,6671	0,5919
12399	HELD_MAL_ADR5ULN	0,0204	0,0336	0,0287	0,0338	0,0497	0,0552
12399	HELD_MAL_ADR3ULN	0,0366	0,0602	0,0433	0,0568	0,0858	0,0714
12399	HELD_ALL_ADR	0,1174	0,109	0,1156	0,0393	0,0481	0,0386
12554	HELD_MAL_ADR	0,0489	0,0266	0,0384	0,0217	0,0303	0,0198
12554	HELD_FEM_VEFF	0,0785	0,0754	0,0774	0,0335	0,0365	0,0329
12851	HELD_FEM_ADR5ULN	0,0841	0,0704	0,087	0,0401	0,0635	0,0488
12851	HELD_MAL_ADR	0,0496	0,0509	0,0432	0,6573	0,6625	0,6573
13025	HELD_MAL_ADR3ULN	0,0572	0,0578	0,0424	0,8568	1	0,8564
13025	HELD_FEM_ADR5ULN	0,0508	0,0491	0,0749	0,2494	0,3182	0,2546
13191	HELD_ALL_CC	0,0795	0,0789	0,0666	0,0287	0,0329	0,0278
13192	HELD_MAL_ADR3ULN	0,0028	0,0047	0,0052	0,2629	0,3274	0,2753
13192	HELD_MAL_ADR5ULN	0,0306	0,0985	0,1047	0,6516	0,7437	0,6584
13192	HELD_ALL_ADR3ULN	0,0459	0,0411	0,0633	0,9559	1	0,9559
13192	HELD_MAL_ADR	0,0927	0,0909	0,0428	0,7098	0,743	0,7097
13193	HELD_MAL_ADR3ULN	0,0022	0,0038	0,0046	0,2596	0,3258	0,2719

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
13193	HELD_MAL_ADR5ULN	0,0227	0,0881	0,1013	0,5694	0,7373	0,5794
13193	HELD_ALL_ADR3ULN	0,0375	0,0347	0,0515	0,9356	1	0,9355
13338	HELD_FEM_UEFF	0,0314	0,033	0,0259	0,5721	0,5935	0,5716
13338	HELD_FEM_VEFF	0,0306	0,0309	0,03	0,8319	0,8624	0,8319
13339	HELD_MAL_ADR	0,0352	0,036	0,011	0,4768	0,5694	0,4767
13339	CVD_FEM	0,1362	0,0953	0,1082	0,0512	0,0803	0,0465
13340	HELD_FEM_VEFF	0,0158	0,0143	0,0137	0,0082	0,0095	0,0072
13479	HELD_FEM_UEFF	0,1063	0,0953	0,1076	0,0341	0,0364	0,0351
13633	HELD_FEM_ADR3ULN	0,0913	0,0763	0,1042	0,0317	0,037	0,0361
13633	HELD_FEM_ADR	0,1138	0,1293	0,1084	0,0387	0,0448	0,0384
13929	HELD_MAL_ADR5ULN	0,2957	0,2981	0,1308	0,1262	0,2119	0,0423
14065	HELD_FEM_EFF	0,087	0,0675	0,0858	0,0307	0,037	0,0303
14083	HELD_FEM_ADR	0,069	0,0657	0,0318	0,0353	0,0459	0,034
14085	HELD_FEM_EFF	0,0345	0,0318	0,0334	0,1267	0,1326	0,126
14087	HELD_FEM_EFF	0,0509	0,0493	0,0504	0,1138	0,1184	0,1138
14102	HELD_MAL_ADR5ULN	0,0062	0,0084	0,0014	0,8445	1	0,844
14102	HELD_FEM_EFF	0,1217	0,124	0,1207	0,0351	0,0391	0,035
14103	HELD_FEM_EFF	0,003	0,0023	0,0004	0,0567	0,0623	0,0565
14103	HELD_FEM_VEFF	0,0371	0,0337	0,0117	0,495	0,5329	0,4948
14103	HELD_FEM_UEFF	0,0605	0,0655	0,0291	0,0747	0,0807	0,076
14129	HELD_ALL_ADR3ULN	0,0384	0,0376	0,0479	0,1413	0,1647	0,1434
14129	HELD_MAL_ADR3ULN	0,0448	0,04	0,0567	0,3415	0,4056	0,3453
14326	HELD_FEM_EFF	0,1463	0,1445	0,1434	0,0461	0,0471	0,0457
14503	HELD_ALL_ADR5ULN	0,0052	0,0046	0,0021	0,6567	0,7349	0,6547
14503	HELD_ALL_ADR3ULN	0,0046	0,0045	0,004	0,5974	0,6922	0,5986
14503	HELD_FEM_ADR5ULN	0,0136	0,0123	0,0063	0,9862	1	0,9862
14503	HELD_FEM_ADR3ULN	0,0203	0,0189	0,0179	0,482	0,5051	0,4834
14537	HELD_ALL_ADR	0,0148	0,0153	0,0133	0,0049	0,0053	0,0048
14537	HELD_FEM_ADR	0,0395	0,0398	0,0332	0,0288	0,0309	0,0284
15915	HELD_FEM_ADR	0,0018	0,0013	0,0012	0,6403	0,6575	0,6405
15915	HELD_ALL_ADR	0,0037	0,0031	0,0029	0,4718	0,5008	0,4719
15915	HELD_ALL_ADR3ULN	0,1292	0,1365	0,0778	0,0267	0,0357	0,021

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
19289	HELD_MAL_CC	0,0256	0,0181	0,0109	0,1599	0,2059	0,1642
19289	HELD_ALL_CC	0,0392	0,0216	0,0288	0,0989	0,1133	0,095
19289	HELD_MAL_LIP	0,0974	0,0892	0,0855	0,0474	0,0689	0,0515
36958	HELD_MAL_ADR3ULN	0,0804	0,108	0,0242	0,0926	0,1218	0,0274
37158	HELD_ALL_ADR	0,0266	0,0259	0,0248	0,0076	0,0078	0,0074
37158	HELD_FEM_ADR	0,0547	0,0511	0,047	0,0328	0,0384	0,0323
37160	HELD_FEM_UEFF	0,0494	0,0385	0,0291	0,0206	0,0238	0,0215
37412	HELD_FEM_ADR5ULN	0,0274	0,0301	0,0228	0,0901	0,1029	0,0965
37412	HELD_ALL_ADR5ULN	0,0463	0,0416	0,0443	0,1444	0,1838	0,1518
37412	HELD_FEM_ADR3ULN	0,1388	0,1374	0,1428	0,0436	0,0523	0,0457
37457	CVD_ALL	0,006	0,0043	0,0045	0,0004	0,0006	0,0005
37457	CVD_FEM	0,0618	0,0475	0,0371	0,0084	0,0138	0,0049
37457	CVD_MAL	0,1106	0,1397	0,1478	0,0425	0,0646	0,0633
37704	HELD_MAL_ADR5ULN	0,0093	0,1304	0,041	0,0096	0,1304	0,0423
38959	CVD_ALL	0,0357	0,0284	0,0234	0,7204	0,8145	0,7186
38959	HELD_FEM_EFF	0,0937	0,0903	0,0433	0,1155	0,1245	0,1149
39292	HELD_FEM_ADR5ULN	0,0461	0,0797	0,1143	0,0295	0,0406	0,0445
39292	HELD_ALL_ADR5ULN	0,2107	0,197	0,2673	0,0487	0,0566	0,0656
39698	HELD_MAL_ADR3ULN	0,0549	0,0575	0,0339	0,1964	0,2316	0,1955
39756	HELD_FEM_ADR3ULN	0,1838	0,1894	0,1779	0,0494	0,069	0,0449
39951	HELD_MAL_ADR	0,0126	0,0133	0,0027	0,1824	0,227	0,1816
39951	HELD_ALL_ADR	0,0036	0,0033	0,0031	0,7179	0,7614	0,7178
39951	HELD_FEM_ADR	0,0243	0,023	0,0233	0,0941	0,102	0,0932
39951	HELD_FEM_ADR5ULN	0,0673	0,0646	0,0583	0,0366	0,0423	0,0421
40466	HELD_FEM_EFF	0,0024	0,002	0,0009	0,0045	0,0058	0,0044
40466	HELD_FEM_UEFF	0,0802	0,0728	0,0265	0,0419	0,0518	0,0382
40466	HELD_FEM_VEFF	0,0511	0,0458	0,0386	0,0313	0,0339	0,0309
44442	HELD_MAL_ADR5ULN	0,0836	0,079	0,0743	0,0364	0,0585	0,0418
55504	HELD_MAL_ADR	0,0719	0,0735	0,0691	0,0286	0,0345	0,0284
55542	HELD_FEM_ADR	0,0351	0,0377	0,0327	0,0223	0,0271	0,0221
55670	HELD_FEM_VEFF	0,0177	0,0252	0,0172	0,0215	0,03	0,0208
55736	HELD_ALL_ADR5ULN	0,0576	0,0583	0,0098	0,0205	0,0356	0,0023

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
55736	HELD_MAL_ADR5ULN	0,0618	0,087	0,0194	0,0901	0,1202	0,0263
55736	HELD_FEM_ADR5ULN	0,3245	0,4065	0,1534	0,1163	0,2053	0,0385
55748	HELD_MAL_ADR5ULN	0,3118	0,3008	0,1412	0;134	0,2136	0,0461
55813	HELD_ALL_ADR3ULN	0,0935	0,0976	0,0867	0,0234	0,0248	0,0235
55845	HELD_FEM_VEFF	0,026	0,0242	0,0254	0,0129	0,0138	0,0128
55845	HELD_MAL_ADR3ULN	0,0952	0,0988	0,0453	0,0432	0,0619	0,0372
55845	HELD_FEM_UEFF	0,1378	0,142	0,1358	0,045	0,0588	0,0453
55923	HELD_FEM_ADR	0,0587	0,058	0,0556	0,0191	0,0224	0,0187
55923	HELD_FEM_ADR3ULN	0,0606	0,0562	0,0659	0,0213	0,0267	0,0222
55945	HELD_FEM_ADR	0,0125	0,0109	0,0112	0,0031	0,0035	0,003
55945	HELD_FEM_ADR3ULN	0,0381	0,0379	0,0442	0,0127	0,0185	0,0137
55945	HELD_ALL_ADR	0,0809	0,0801	0,0782	0,0292	0,0327	0,029
56007	HELD_MAL_ADR3ULN	0,0308	0,0293	0,005	0,1915	0,2107	0,1828
56007	HELD_MAL_ADR5ULN	0,139	0,1477	0,0466	0,2654	0,2957	0,2514
56011	HELD_ALL_ADR5ULN	0,1056	0,2178	0,0322	0,1135	0,2277	0,0343
56104	HELD_FEM_UEFF	0,0155	0,0153	0,0149	0,0164	0,0198	0,0166
56113	HELD_ALL_ADR5ULN	0,0186	0,0163	0,0264	0,0347	0,0387	0,0352
56113	HELD_ALL_ADR3ULN	0,0285	0,029	0,0276	0,3219	0,3794	0,3228
56113	HELD_FEM_ADR5ULN	0,0402	0,0472	0,0536	0,036	0,0498	0,0358
56113	HELD_FEM_ADR3ULN	0,0416	0,0401	0,0432	0,1311	0,1519	0,1314
56636	HELD_FEM_ADR	0,0108	0,0106	0,0098	0,5577	0,6169	0,5576
56636	HELD_FEM_ADR3ULN	0,0227	0,0223	0,0215	0,7019	0,7532	0,7016
56636	HELD_FEM_ADR5ULN	0,0271	0,0247	0,027	0,8077	0,8498	0,8079
56666	HELD_MAL_ADR3ULN	0,2121	0,3446	0,0763	0,0154	0,0133	0,0018
56666	HELD_MAL_ADR5ULN	0,3794	0,418	0,1913	0,0556	0,0716	0,0122
56666	HELD_MAL_ADR	0,1717	0,119	0,136	0,0173	0,0265	0,0154
56667	HELD_FEM_EFF	0,0364	0,0372	0,0356	0,0134	0,014	0,0133
56667	HELD_MAL_ADR3ULN	0,2981	0,4124	0,2471	0,0382	0,0579	0,0311
56667	HELD_FEM_ADR3ULN	0,1228	0,1267	0,1124	0,0483	0,0586	0,0492
56780	HELD_FEM_ADR3ULN	0,0149	0,0159	0,008	0,012	0,0164	0,0117
56780	HELD_FEM_ADR	0,0227	0,0214	0,0192	0,012	0,0154	0,0118
56780	HELD_ALL_ADR3ULN	0,0269	0,0274	0,019	0,0143	0,0182	0,0141

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
56780	HELD_ALL_ADR	0,0842	0,0843	0,0808	0,0435	0,0453	0,0433
56876	HELD_FEM_UEFF	0,0372	0,0266	0,0308	0,0169	0,0232	0,0141
56876	HELD_FEM_EFF	0,0424	0,0386	0,0418	0,0166	0,0177	0,0163
56876	HELD_FEM_VEFF	0,0713	0,0569	0,0692	0,0196	0,0216	0,0192
56978	HELD_ALL_ADR5ULN	0,0719	0,0767	0,0535	0,0154	0,0156	0,0118
57000	HELD_FEM_VEFF	0,0174	0,0176	0,0169	0,3734	0,4158	0,3731
57000	HELD_FEM_UEFF	0,0415	0,0406	0,0369	0,858	0,8914	0,8579
57000	CVD_ALL	0,0418	0,0488	0,0445	0,0607	0,0713	0,0637
57000	CVD_MAL	0,0441	0,0754	0,0552	0,1657	0,2666	0,1782
57313	HELD_FEM_UEFF	0,034	0,0307	0,0344	0,1193	0,15	0,1201
57734	HELD_FEM_ADR3ULN	0,1496	0,1859	0,1593	0,0475	0,0622	0,0534
57837	HELD_MAL_ADR3ULN	0,1875	0,2505	0,1226	0,0606	0,0663	0,0405
57853	HELD_FEM_EFF	0,0026	0,0022	0,0012	0,0086	0,0107	0,0084
57853	HELD_FEM_UEFF	0,0504	0,0448	0,0138	0,0301	0,0444	0,0274
57853	HELD_FEM_VEFF	0,042	0,0386	0,0288	0,0505	0,0562	0,0501
57854	HELD_FEM_EFF	0,0212	0,0209	0,0157	0,0665	0,0761	0,0663
57854	HELD_FEM_UEFF	0,0736	0,0661	0,0242	0,0496	0,068	0,0464
57854	HELD_MAL_ADR3ULN	0,1957	0,2011	0,1232	0,0634	0,0859	0,0467
58295	HELD_MAL_ADR	0,0215	0,0221	0,0192	0,0596	0,0793	0,0593
58402	HELD_MAL_ADR3ULN	0,253	0,3601	0,2207	0,0277	0,0317	0,0255
58407	HELD_FEM_VEFF	0,009	0,0089	0,0086	0,6756	0,7344	0,6756
58407	HELD_FEM_UEFF	0,0269	0,0254	0,019	0,1833	0,1983	0,1819
58440	HELD_FEM_UEFF	0,1021	0,1012	0,1022	0,0294	0,0358	0,0305
58525	HELD_FEM_ADR	0,0008	0,0004	0,0004	0,0002	0,0003	0,0001
58525	HELD_FEM_ADR3ULN	0,0005	0,0002	0,0008	0,0002	0,0006	0,0005
58525	HELD_FEM_ADR5ULN	0,0002	0,0005	0,0011	0,0009	0,0042	0,0034
58525	HELD_ALL_ADR	0,0309	0,0274	0,0284	0,0041	0,005	0,0037
58525	HELD_ALL_ADR5ULN	0,0115	0,0352	0,0209	0,0263	0,0423	0,0412
58525	HELD_ALL_ADR3ULN	0,0304	0,0391	0,0408	0,0158	0,0198	0,021
58533	HELD_FEM_ADR	0,0132	0,0076	0,011	0,0024	0,0033	0,0019
58533	HELD_FEM_ADR3ULN	0,0373	0,0325	0,0534	0,0101	0,0153	0,0155
58533	HELD_FEM_ADR5ULN	0,0255	0,0368	0,0556	0,0387	0,0613	0,0658

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
58533	HELD_ALL_ADR	0,1948	0,2046	0,1921	0,0446	0,0584	0,0438
58544	HELD_MAL_ADR5ULN	0,2134	0,1955	0,0875	0,0754	0,1197	0,02
58716	HELD_MAL_ADR3ULN	0,0222	0,0288	0,011	0,0012	0,0018	0,0003
58716	HELD_MAL_ADR5ULN	0,1918	0,256	0,1602	0,0649	0,0886	0,047
58736	HELD_FEM_EFF	0,0378	0,0385	0,0374	0,0117	0,0131	0,0117
58808	HELD_FEM_ADR	0,0754	0,076	0,0739	0,0276	0,0333	0,0275
58809	HELD_MAL_ADR5ULN	0,1338	0,1368	0,0404	0,0454	0,0777	0,0088
58809	HELD_ALL_ADR3ULN	0,0117	0,011	0,0202	0,0915	0,1137	0,099
58809	HELD_MAL_ADR3ULN	0,0206	0,0207	0,0247	0,2401	0,3238	0,253
58809	HELD_FEM_UEFF	0,1023	0,1072	0,0586	0,0482	0,0528	0,0446
58886	HELD_FEM_ADR3ULN	0,0432	0,0444	0,0387	0,0115	0,0145	0,0107
58886	HELD_ALL_ADR3ULN	0,0611	0,0627	0,0549	0,0171	0,0233	0,0168
58886	HELD_ALL_ADR5ULN	0,1212	0,1272	0,097	0,0433	0,049	0,0427
58926	HELD_MAL_ADR3ULN	0,0186	0,0222	0,0152	0,0031	0,005	0,0036
58926	HELD_ALL_ADR5ULN	0,0504	0,0525	0,0476	0,0108	0,0121	0,0117
58926	CVD_FEM	0,0461	0,0455	0,0419	0,7899	0,8184	0,7899
58926	HELD_MAL_ADR5ULN	0,1263	0,1409	0,1002	0,0427	0,0517	0,0487
58968	HELD_ALL_ADR5ULN	0,0212	0,0248	0,0199	0,0023	0,003	0,003
58968	HELD_MAL_ADR3ULN	0,0412	0,0375	0,0377	0,0067	0,0098	0,0085
58968	HELD_ALL_ADR3ULN	0,1321	0,1309	0,1338	0,0208	0,028	0,0226
58968	HELD_FEM_ADR5ULN	0,1447	0,1579	0,1408	0,0233	0,0292	0,0261
58985	HELD_ALL_ADR5ULN	0,0341	0,0303	0,0449	0,0085	0,0129	0,0104
59113	HELD_MAL_ADR5ULN	0,0156	0,0224	0,0114	0,0006	0,0008	0,0003
59113	HELD_MAL_ADR3ULN	0,0577	0,0875	0,0558	0,0073	0,009	0,0068
59236	HELD_ALL_ADR	0,0163	0,0158	0,0148	0,0638	0,077	0,0636
59236	HELD_ALL_ADR3ULN	0,0152	0,0151	0,017	0,3664	0,3858	0,3685
59236	HELD_FEM_ADR	0,0242	0,0266	0,0221	0,0693	0,0722	0,0689
59237	HELD_FEM_VEFF	0,021	0,0197	0,0205	0,9766	1	0,9766
59237	HELD_FEM_EFF	0,0278	0,0283	0,0273	0,5742	0,6002	0,5742
59267	HELD_FEM_UEFF	0,0007	0,0006	0,0005	0,0035	0,0042	0,0036
59352	HELD_MAL_ADR	0,0234	0,0233	0,0219	0,6204	0,6787	0,6203
59352	HELD_ALL_ADR	0,0427	0,0412	0,0406	0,8742	0,925	0,8742

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
59363	CVD_MAL	0,0678	0,0736	0,0797	0,0336	0,0422	0,0351
59368	HELD_FEM_ADR	0,0119	0,0127	0,0096	0,0049	0,0053	0,0048
59371	HELD_FEM_VEFF	0,0024	0,0022	0,0021	0,1509	0,1694	0,1508
59371	HELD_FEM_UEFF	0,0098	0,0099	0,0092	0,2681	0,286	0,2686
59372	HELD_MAL_ADR	0,1687	0,1722	0,1609	0,0282	0,042	0,0273
59372	HELD_MAL_ADR3ULN	0,22	0,2638	0,2592	0,0467	0,0804	0,0599
59443	HELD_ALL_ADR5ULN	0,0027	0,0031	0,0018	0,366	0,4699	0,3621
59443	HELD_MAL_ADR5ULN	0,0416	0,036	0,0368	0,877	1	0,877
900080	HELD_FEM_ADR3ULN	0,0248	0,0243	0,0334	0,0078	0,0122	0,011
900080	HELD_FEM_ADR5ULN	0,0307	0,0334	0,0528	0,0422	0,0571	0,0639
900102	HELD_FEM_UEFF	0,0079	0,0078	0,008	0,0043	0,0057	0,0041
900102	HELD_FEM_VEFF	0,0423	0,0413	0,0416	0,0163	0,0185	0,0162
900111	HELD_FEM_UEFF	0,022	0,0232	0,0222	0,0107	0,012	0,0103
900111	HELD_FEM_VEFF	0,0524	0,0496	0,0516	0,0293	0,0351	0,0292
900117	HELD_MAL_LIP	0,049	0,0534	0,022	0,0073	0,0136	0,0043
900118	HELD_FEM_EFF	0,0013	0,0008	0,001	0,0001	0,0002	0,0001
900118	HELD_FEM_VEFF	0,1013	0,0874	0,0978	0,0214	0,0303	0,0206
900118	HELD_FEM_ADR5ULN	0,0424	0,0506	0,0251	0,8579	1	0,8561
900118	HELD_ALL_ADR5ULN	0,0702	0,0623	0,0401	0,653	0,7517	0,6608
900120	HELD_FEM_EFF	0,0101	0,0092	0,007	0,0095	0,0109	0,0093
900121	HELD_FEM_EFF	0,0944	0,0944	0,0922	0,0477	0,0488	0,0476
900123	HELD_ALL_ADR	0,0402	0,0568	0,0164	0,041	0,0576	0,0168
900123	HELD_FEM_ADR	0,0678	0,1074	0,0341	0,0695	0,1089	0,0349
900124	HELD_FEM_EFF	0,0185	0,0181	0,0177	0,0602	0,0663	0,0601
900132	HELD_FEM_ADR	0,0215	0,0178	0,0068	0,2283	0,2679	0,2288
900144	CVD_FEM	0,0319	0,0744	0,0093	0,0361	0,0813	0,0104
900144	HELD_ALL_ADR5ULN	0,1356	0,2119	0,0476	0,1425	0,2202	0,0497
900145	CVD_FEM	0,0702	0,0367	0,0231	0,4142	0,4698	0,4044
900145	HELD_ALL_ADR5ULN	0,1364	0,2117	0,0481	0,1436	0,2203	0,0504
900146	HELD_FEM_ADR5ULN	0,0096	0,017	0,0195	0,0366	0,0413	0,0447
900146	HELD_FEM_CC	0,0751	0,0844	0,0429	0,4385	0,4606	0,4405
900146	HELD_MAL_ADR	0,1074	0,1347	0,0497	0,2672	0,3098	0,2671

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
900147	HELD_ALL_ADR3ULN	0,0572	0,0567	0,0416	0,0133	0,015	0,0104
900147	HELD_FEM_ADR3ULN	0,0435	0,0527	0,0381	0,0166	0,0182	0,0127
900196	HELD_MAL_LIP	0,04	0,0376	0,0365	0,0037	0,0057	0,0039
900196	HELD_FEM_LIP	0,0183	0,019	0,0214	0,0168	0,0301	0,0136
900196	HELD_FEM_ADR3ULN	0,0672	0,0693	0,022	0,0238	0,0276	0,0198
900196	CVD_FEM	0,0398	0,0432	0,0293	1	1	1
900196	CVD_ALL	0,0617	0,0655	0,0425	0,1649	0,2139	0,1618
900200	CVD_FEM	0,0865	0,0948	0,0822	0,0359	0,0545	0,0381
900204	HELD_FEM_EFF	0,0051	0,0054	0,005	0,0195	0,0204	0,0194
900205	HELD_FEM_EFF	0,0128	0,0126	0,0126	0,0746	0,0753	0,0745
900205	CVD_MAL	0,0881	0,0873	0,0279	0,0497	0,0672	0,045
900223	HELD_FEM_ADR	0,1823	0,2018	0,1522	0,0357	0,0826	0,0327
900225	HELD_ALL_ADR5ULN	0,0532	0,0765	0,011	0,0615	0,0864	0,0125
900225	HELD_MAL_ADR3ULN	0,0804	0,108	0,0242	0,0926	0,1218	0,0274
900227	HELD_FEM_ADR5ULN	0,076	0,0933	0,0368	0,0271	0,031	0,0108
900233	HELD_FEM_ADR5ULN	0,0314	0,0303	0,024	0,3185	0,3387	0,3136
900236	HELD_FEM_ADR3ULN	0,0378	0,0275	0,0387	0,0494	0,064	0,0568
900236	HELD_MAL_ADR5ULN	0,2375	0,2927	0,0919	0,0994	0,13	0,0289
900241	HELD_FEM_EFF	0,0225	0,0223	0,0219	0,6377	0,6538	0,6376
900242	HELD_ALL_ADR5ULN	0,0164	0,0165	0,0012	0,0015	0,0017	0
900242	HELD_ALL_ADR3ULN	0,0158	0,0151	0,0031	0,0007	0,0006	0,0002
900242	HELD_FEM_ADR5ULN	0,0257	0,0467	0,0032	0,0088	0,0105	0,0007
900242	HELD_MAL_ADR3ULN	0,1963	0,3073	0,0673	0,0132	0,0144	0,0014
900242	HELD_FEM_ADR	0,0219	0,0117	0,0142	0,006	0,0067	0,0053
900242	HELD_FEM_ADR3ULN	0,0542	0,0556	0,0305	0,0161	0,0247	0,0091
900242	HELD_ALL_ADR	0,0373	0,0359	0,0352	0,0146	0,0152	0,0142
900242	HELD_MAL_ADR5ULN	0,416	0,4311	0,2189	0,0691	0,1332	0,0165

Table 6a **Correlation of genotypes of PA SNPs to relative risk**

For diagnostic conclusions to be drawn from genotyping a particular patient we calculated the relative risk RR1, RR2, RR3 for the three possible genotypes of each SNP. Given the genotype frequencies as

	gtype1	gtype2	gtype3
case	N11	N12	N13
control	N21	N22	N23

we calculate

$$\boxed{RR1 = \frac{N11}{N21} \Big/ \frac{N12 + N13}{N22 + N23}}$$

$$\boxed{RR2 = \frac{N12}{N22} \Big/ \frac{N11 + N13}{N21 + N23}}$$

$$\boxed{RR3 = \frac{N13}{N23} \Big/ \frac{N11 + N12}{N21 + N22}}$$

Here, the *case* and *control* populations represent any case-control-group pair, or bad(case)-good(control)-group pair, respectively (due to their increased response to statins, 'high responders' are treated as a case cohort, whereas 'low responders' are treated as the respective control cohort). A value RR1>1, RR2>1, and RR3>1 indicates an increased risk for individuals carrying genotype 1, genotype 2, and genotype 3, respectively. For example, RR1=3 indicates a 3-fold risk of an individual carrying genotype 1 as compared to individuals carrying genotype 2 or 3 (a detailed description of relative risk calculation and statistics can be found in (Biostatistics, L. D. Fisher and G. van Belle, Wiley Interscience 1993)). The baySNP number refers to an internal numbering of the PA SNPs and can be found in the sequence listing. null: not defined.

In cases where a relative risk is not given in the table (three times zero or null) the informative genotype can be drawn from the right part of the table where the frequencies of genotypes are given in the cases and control cohorts. For example BaySNP 3360 gave the following results:

BAYSNP	COMPARISON	GTYPE1	GTYPE2	GTYPE3	RR1	RR2	RR3
3360	HELD_MAL_ADR5ULN	GG	GT	TT	null	0	0

FQ1_A	FQ2_A	FQ3_A	FQ1_B	FQ2_B	FQ3_B
10	0	0	50	22	1

It can be concluded that a GT or TT genotype is only present in the control cohort; these genotypes are somehow protective against ADR. An analogous proceeding can be used to determine protective alleles if no relative risk is given (table 6b).

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
29	A	G	HELD_FEM_LIP	1,26	0,79	80	100	60	78	80	76
29	A	G	HELD_ALL_ADR3ULN	1,33	0,75	47	54	40	131	125	137
29	A	G	HELD_ALL_LIP	1,23	0,81	99	122	76	114	119	109
52	C	G	HELD_ALL_CC	0,63	1,6	43	42	44	39	57	21
52	C	G	HELD_MAL_HDL	0,94	1,06	18	20	16	25	29	21
52	C	G	HELD_FEM_CC	0,69	1,45	29	27	31	22	30	14
52	C	G	HELD_MAL_CC	0,55	1,82	14	15	13	17	27	7
52	C	G	HELD_MAL_LIP2	0,88	1,14	253	254	252	281	317	245
57	C	T	HELD_FEM_CC	0,62	1,62	31	45	17	22	41	3
118	C	T	HELD_MAL_LIP2	1,16	0,86	306	493	119	337	512	162
137	G	A	HELD_MAL_ADR5ULN	0,46	2,18	8	7	9	54	71	37
137	G	A	HELD_ALL_ADR5ULN	0,73	1,37	23	25	21	119	151	87
137	G	A	HELD_ALL_ADR3ULN	0,72	1,39	44	46	42	119	151	87
179	G	A	HELD_MAL_ADR5ULN	1,07	0,93	8	14	2	56	97	15
179	G	A	HELD_MAL_ADR3ULN	1,38	0,72	16	29	3	56	97	15
179	G	A	HELD_ALL_ADR5ULN	1,16	0,86	25	45	5	124	219	29
179	G	A	HELD_ALL_ADR	1,2	0,84	128	234	22	124	219	29
240	G	C	HELD_ALL_ADR3ULN	2,22	0,45	44	83	5	130	224	36
240	G	C	HELD_MAL_ADR3ULN	4,16	0,24	17	33	1	59	102	16
241	G	A	HELD_ALL_ADR3ULN	0,66	1,51	47	60	34	129	196	62
241	G	A	HELD_ALL_ADR5ULN	0,58	1,72	25	31	19	129	196	62
241	G	A	HELD_MAL_ADR3ULN	0,54	1,84	17	19	15	58	86	30

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
288	G	C	CVD_ALL	0,82	1,22	101	146	56	73	119	27
384	C	G	CVD_ALL	1,13	0,89	104	123	85	74	77	71
384	C	G	HELD_FEM_CC	1,47	0,68	31	38	24	22	17	27
533	G	A	CVD_ALL	0,8	1,25	103	162	44	74	129	19
542	G	A	HELD_FEM_ADR	0,78	1,28	73	118	28	71	125	17
576	C	T	HELD_ALL_LIP	null	0	100	200	0	115	225	5
576	C	T	HELD_FEM_LIP	null	0	81	162	0	79	154	4
608	G	A	CVD_MAL	1,57	0,64	68	120	16	33	47	19
614	G	A	HELD_MAL_HDL	6,2	0,16	20	30	10	26	0	52
614	G	A	HELD_ALL_CC	0,65	1,53	44	57	31	40	67	13
614	G	A	HELD_MAL_CC	0,47	2,12	13	12	14	18	28	8
614	G	A	HELD_MAL_LIP	0,52	1,92	19	21	17	35	55	15
614	G	A	CVD_ALL	0,8	1,25	96	126	66	63	98	28
614	G	A	HELD_FEM_CC	0,69	1,44	31	45	17	22	39	5
738	A	C	CVD_ALL	0,82	1,22	104	106	102	74	93	55
1056	A	G	HELD_ALL_HDL	1,58	0,63	34	51	17	50	59	41
1056	A	G	HELD_FEM_LIP	0,81	1,24	78	98	58	78	113	43
1092	G	C	HELD_MAL_ADR5ULN	1,28	0,78	8	12	4	59	82	36
1524	C	A	HELD_MAL_CC2	0,7	1,43	44	56	32	26	44	8
1524	C	A	HELD_ALL_LIP	1,28	0,78	96	151	41	112	158	66
1524	C	A	HELD_ALL_CC	1,52	0,66	44	72	16	39	52	26
1574	T	C	CVD_MAL	1,15	0,87	69	119	19	34	55	13

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
1582	T	C	HELD_MAL_ADR3ULN	3,32	0,3	16	30	2	53	83	23
1657	C	T	HELD_FEM_EFF	1,19	0,84	23	29	17	33	37	29
1722	T	C	CVD_MAL	1,1	0,91	63	79	47	33	37	29
1756	C	T	HELD_MAL_ADR5ULN	0,36	2,81	9	14	4	56	104	8
1757	G	A	HELD_ALL_CC	0,87	1,15	45	63	27	38	58	18
1757	G	A	HELD_FEM_CC	0,77	1,3	31	40	22	21	33	9
1757	G	A	HELD_FEM_VEFF	0,84	1,19	148	177	119	152	206	98
1757	G	A	HELD_MAL_ADR	0,94	1,06	62	90	34	58	87	29
1765	A	G	HELD_ALL_LIP	0,86	1,16	100	29	171	107	39	175
1767	T	C	HELD_ALL_ADR3ULN	2,85	0,35	40	75	5	107	172	42
1767	T	C	HELD_ALL_ADR5ULN	4,15	0,24	21	40	2	107	172	42
1767	T	C	HELD_MAL_ADR5ULN	0	null	7	0	14	53	86	20
1767	T	C	HELD_FEM_ADR3ULN	2,39	0,42	27	50	4	54	86	22
1767	T	C	HELD_MAL_ADR3ULN	4,73	0,21	13	25	1	53	86	20
1837	C	T	HELD_ALL_ADR3ULN	1,61	0,62	48	75	21	132	173	91
1837	C	T	HELD_FEM_LIP	1,14	0,88	81	120	42	79	109	49
1837	C	T	HELD_ALL_LIP	1,11	0,9	100	145	55	115	158	72
1837	C	T	HELD_ALL_ADR	1,19	0,84	134	195	73	132	173	91
1854	A	G	HELD_FEM_LIP	0,81	1,23	80	85	75	79	100	58
1862	C	T	HELD_FEM_LIP	1,34	0,75	80	121	39	76	97	55
2085	G	T	HELD_FEM_CC	1,6	0,62	31	44	18	22	20	24
2085	G	T	HELD_ALL_CC	1,44	0,7	45	61	29	40	40	40

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
2093	C	T	HELD_MAL_CC	0,42	2,4	14	15	13	18	32	4
2093	C	T	HELD_ALL_CC	0,73	1,38	45	62	28	40	66	14
2109	A	G	HELD_MAL_HDL	2,22	0,45	19	34	4	22	31	13
2109	A	G	HELD_ALL_HDL	1,68	0,6	39	70	8	48	76	20
2109	A	G	HELD_ALL_LIP2	1,14	0,88	624	1035	213	700	1109	291
2109	A	G	HELD_FEM_LIP	1,46	0,69	80	139	21	78	120	36
2124	G	T	HELD_MAL_LIP	0,57	1,75	17	14	20	32	40	24
2140	G	T	HELD_FEM_UEFF	2,15	0,46	43	79	7	60	94	26
2140	G	T	HELD_FEM_EFF	1,3	0,77	237	416	58	239	390	88
2140	G	T	HELD_MAL_ADR	1,61	0,62	46	80	12	49	73	25
2140	G	T	HELD_FEM_VEFF	1,35	0,74	119	207	31	122	194	50
2141	G	A	HELD_MAL_ADR3ULN	3,89	0,26	16	30	2	52	78	26
2141	G	A	HELD_FEM_UEFF	1,37	0,73	53	91	15	77	121	33
2141	G	A	HELD_MAL_ADR	1,47	0,68	58	100	16	52	78	26
2186	T	C	HELD_MAL_ADR5ULN	0,37	2,7	9	14	4	59	109	9
2187	C	T	HELD_FEM_ADR3ULN	0,65	1,54	30	37	23	71	107	35
2192	G	A	HELD_FEM_ADR	7,27	0,14	69	137	1	70	127	13
2192	G	A	HELD_FEM_ADR3ULN	0	null	30	0	60	70	127	13
2192	G	A	HELD_ALL_ADR	2,19	0,46	132	258	6	126	233	19
2192	G	A	HELD_FEM_ADR5ULN	0	null	16	0	32	70	127	13
2192	G	A	HELD_ALL_ADR3ULN	2,97	0,34	47	92	2	126	233	19
2203	T	C	HELD_FEM_LIP	0,74	1,35	80	106	54	79	125	33

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
2203	T	C	HELD_ALL_LIP	0,8	1,25	98	128	68	115	171	59
2217	G	T	HELD_MAL_CC	0,46	2,17	13	14	12	17	29	5
2217	G	T	CVD_FEM	2,4	0,42	33	63	3	40	68	12
2281	A	C	HELD_FEM_CC	0,64	1,55	31	26	36	22	30	14
2281	A	C	HELD_MAL_CC	1,71	0,58	14	20	8	18	18	18
2284	G	A	HELD_MAL_LIP	3,58	0,28	17	32	2	35	53	17
2290	A	G	HELD_MAL_CC	0,42	2,41	14	18	10	18	34	2
2327	A	C	HELD_MAL_ADR	1,24	0,8	59	70	48	54	52	56
2327	A	C	HELD_MAL_ADR5ULN	1,57	0,64	9	11	7	54	52	56
2327	A	C	HELD_MAL_ADR3ULN	1,68	0,59	17	22	12	54	52	56
2327	A	C	HELD_FEM_EFF	0,9	1,11	270	249	291	281	287	275
2353	A	G	CVD_MAL	0,74	1,36	66	117	15	21	42	0
2353	A	G	HELD_ALL_CC	1,62	0,62	45	83	7	38	63	13
2353	A	G	CVD_ALL	0,77	1,29	100	178	22	49	94	4
2353	A	G	HELD_FEM_CC	1,54	0,65	31	58	4	21	36	6
2371	A	C	HELD_ALL_LIP2	0,91	1,1	630	927	333	726	1117	335
2376	C	T	HELD_ALL_LIP2	0,79	1,26	620	1193	47	717	1400	34
2401	T	G	HELD_FEM_UEFF	0,77	1,31	52	76	28	73	119	27
2463	T	C	HELD_ALL_CC	11,29	0,09	44	81	7	36	0	72
2463	T	C	HELD_FEM_CC	8,33	0,12	30	54	6	22	0	44
2463	T	C	HELD_FEM_LIP2	0,96	1,04	307	572	42	370	693	47
2755	A	G	HELD_FEM_ADR	0,77	1,31	72	69	75	70	86	54

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
2755	A	G	HELD_ALL_ADR	0,85	1,18	134	147	121	128	162	94
2755	A	G	HELD_FEM_EFF	1,05	0,95	271	331	211	284	333	235
2925	G	A	HELD_FEM_VEFF	1,27	0,79	141	163	119	145	134	156
2925	G	A	HELD_FEM_UEFF	1,48	0,68	54	64	44	77	66	88
3043	G	A	HELD_FEM_ADR3ULN	2,96	0,34	17	32	2	31	49	13
3152	T	A	HELD_FEM_VEFF	1,1	0,91	107	125	89	108	116	100
3214	C	G	HELD_FEM_VEFF	1,09	0,92	151	253	49	142	231	53
3215	C	G	HELD_MAL_ADR5ULN	0,12	8,06	9	17	1	60	120	0
3237	C	G	HELD_FEM_CC	3,84	0,26	28	55	1	18	31	5
3241	T	C	HELD_MAL_ADR	1,4	0,71	45	57	33	51	49	53
3826	C	A	HELD_MAL_ADR5ULN	0	null	7	0	14	44	71	17
3826	C	A	HELD_ALL_ADR5ULN	4,58	0,22	18	35	1	90	156	24
3826	C	A	HELD_MAL_ADR3ULN	4,4	0,23	12	23	1	44	71	17
3842	C	G	CVD_ALL	0,6	1,66	100	190	10	63	126	0
3842	C	G	CVD_MAL	0,68	1,47	68	129	7	30	60	0
3842	C	G	CVD_FEM	0,48	2,08	32	61	3	33	66	0
3843	A	T	HELD_MAL_CC2	1,45	0,69	23	32	14	17	17	17
3843	A	T	HELD_FEM_HDL	0,63	1,59	12	11	13	15	20	10
3869	G	T	HELD_FEM_UEFF	1,46	0,69	53	76	30	73	84	62
3942	C	A	HELD_FEM_UEFF	0,55	1,81	54	91	17	74	141	7
4018	T	C	HELD_MAL_LIP	2,11	0,47	18	30	6	36	46	26
4206	A	T	HELD_ALL_ADR3ULN	0,7	1,43	48	47	49	132	161	103

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
4206	A	T	HELD_FEM_ADR	0,79	1,27	72	72	72	72	89	55
4206	A	T	HELD_ALL_ADR5ULN	0,61	1,65	26	24	28	132	161	103
4527	G	A	CVD_ALL	1,18	0,85	71	114	28	54	80	28
4527	G	A	HELD_FEM_LIP2	1,19	0,84	320	508	132	370	546	194
4527	G	A	HELD_MAL_CC	0,47	2,15	12	17	7	16	30	2
4527	G	A	HELD_MAL_CC2	1,43	0,7	45	71	19	29	36	22
4527	G	A	HELD_ALL_ADR3ULN	0,67	1,5	48	68	28	124	202	46
4527	G	A	HELD_ALL_CC2	1,24	0,81	104	162	46	71	97	45
4527	G	A	HELD_ALL_ADR5ULN	0,59	1,71	26	36	16	124	202	46
4544	G	A	HELD_MAL_ADR3ULN	0,43	2,34	17	20	14	59	97	21
4544	G	A	HELD_MAL_ADR	0,74	1,35	62	87	37	59	97	21
4544	G	A	HELD_ALL_ADR	0,82	1,23	133	183	83	130	201	59
4544	G	A	HELD_ALL_ADR3ULN	0,69	1,44	47	63	31	130	201	59
4545	G	A	HELD_MAL_ADR3ULN	0,43	2,34	17	20	14	59	97	21
4545	G	A	HELD_MAL_ADR	0,73	1,37	61	85	37	59	97	21
4545	G	A	HELD_ALL_ADR	0,82	1,22	132	181	83	128	197	59
4668	C	A	HELD_ALL_ADR5ULN	1,52	0,66	26	34	18	130	139	121
4669	C	T	HELD_FEM_EFF	0,85	1,17	286	474	98	281	490	72
4718	G	A	HELD_MAL_LIP	1,44	0,7	18	26	10	34	41	27
4818	G	A	HELD_MAL_LIP	0,62	1,62	17	20	14	36	54	18
4827	A	G	HELD_MAL_ADR5ULN	0,76	1,31	9	15	3	59	103	15
4838	A	G	HELD_ALL_CC2	1,2	0,83	101	113	89	71	64	78

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
4856	G	A	CVD_MAL	0	null	69	0	138	34	65	3
4868	T	C	HELD_MAL_ADR	0,84	1,19	62	88	36	59	92	26
4868	T	C	HELD_MAL_ADR5ULN	0,66	1,51	8	11	5	59	92	26
4887	C	A	HELD_MAL_CC	3,98	0,25	14	26	2	18	23	13
4887	C	A	HELD_ALL_CC	1,48	0,67	45	75	15	38	53	23
4912	G	A	HELD_MAL_LIP	0,45	2,21	12	7	17	31	34	28
4951	G	A	HELD_ALL_ADR3ULN	0,9	1,11	48	51	45	128	145	111
4951	G	A	HELD_FEM_ADR3ULN	0,78	1,28	31	29	33	69	77	61
4951	G	A	HELD_FEM_ADR5ULN	0,56	1,77	17	13	21	69	77	61
4951	G	A	HELD_ALL_ADR5ULN	0,62	1,62	26	22	30	128	145	111
4951	G	A	HELD_FEM_ADR	0,84	1,2	73	68	78	69	77	61
4951	G	A	HELD_ALL_ADR	0,88	1,14	135	135	135	128	145	111
4952	T	C	HELD_ALL_ADR3ULN	0,93	1,08	48	52	44	128	145	111
4952	T	C	HELD_FEM_ADR3ULN	0,78	1,28	31	30	32	70	80	60
4952	T	C	HELD_FEM_ADR5ULN	0,6	1,68	17	14	20	70	80	60
4952	T	C	HELD_ALL_ADR5ULN	0,66	1,51	26	23	29	128	145	111
4966	G	A	HELD_MAL_LIP	2,11	0,47	18	27	9	34	34	34
4966	G	A	HELD_MAL_ADR	1,24	0,81	61	68	54	59	53	65
4966	G	A	HELD_FEM_CC	0,71	1,4	30	25	35	21	26	16
5019	A	T	CVD_FEM	0,6	1,66	32	25	39	34	43	25
5019	A	T	HELD_ALL_CC2	1,21	0,82	87	96	78	62	54	70
5019	A	T	HELD_MAL_HDL	2,11	0,47	18	27	9	22	20	24

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
5019	A	T	HELD_ALL_LIP	1,33	0,75	86	95	77	100	84	116
5019	A	T	HELD_MAL_CC2	1,43	0,7	37	43	31	24	17	31
5165	C	A	HELD_FEM_ADR3ULN	0,63	1,6	30	46	14	70	122	18
5165	C	A	HELD_MAL_ADR5ULN	0,76	1,31	9	15	3	59	103	15
5165	C	A	HELD_FEM_ADR	0,82	1,21	71	116	26	70	122	18
5165	C	A	HELD_FEM_ADR5ULN	0,53	1,87	16	24	8	70	122	18
5278	G	A	HELD_MAL_ADR5ULN	0,42	2,35	9	10	8	60	93	27
5287	C	T	HELD_FEM_VEFF	0,77	1,29	159	257	61	147	260	34
5320	A	G	CVD_FEM	1,5	0,67	33	40	26	38	32	44
5324	T	C	HELD_FEM_VEFF	0,83	1,2	137	124	150	134	146	122
5373	G	T	HELD_FEM_ADR5ULN	4,01	0,25	16	29	3	71	94	48
5373	G	T	HELD_ALL_ADR5ULN	2,13	0,47	25	42	8	131	180	82
5375	C	T	HELD_FEM_ADR5ULN	4,08	0,25	15	27	3	70	90	50
5375	C	T	HELD_ALL_ADR5ULN	1,88	0,53	24	39	9	128	173	83
5376	A	T	HELD_MAL_ADR5ULN	0,11	8,73	8	15	1	58	116	0
5377	T	C	HELD_FEM_ADR	1,19	0,84	60	88	32	64	85	43
5377	T	C	HELD_FEM_ADR5ULN	2,75	0,36	15	26	4	64	85	43
5517	A	G	HELD_MAL_ADR	1,49	0,67	53	104	2	55	106	4
5518	G	C	HELD_FEM_ADR5ULN	143	0,01	16	31	1	71	0	142
5564	G	T	CVD_MAL	0,85	1,17	69	73	65	34	44	24
5569	G	A	HELD_MAL_ADR5ULN	5,56	0,18	8	15	1	53	74	32
5569	G	A	HELD_ALL_ADR5ULN	2,07	0,48	22	37	7	122	170	74

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
5716	G	C	HELD_ALL_ADR3ULN	0,57	1,74	44	34	54	109	126	92
5716	G	C	HELD_FEM_ADR3ULN	0,5	1,98	29	18	40	59	65	53
5716	G	C	HELD_ALL_ADR5ULN	0,48	2,07	22	16	28	109	126	92
5716	G	C	HELD_FEM_ADR5ULN	0,49	2,05	15	10	20	59	65	53
5717	G	A	HELD_ALL_ADR5ULN	0,59	1,68	26	20	32	132	142	122
5717	G	A	CVD_FEM	0,61	1,64	17	12	22	19	22	16
5850	G	A	HELD_MAL_CC	0,66	1,52	14	14	14	15	21	9
5959	G	A	CVD_MAL	1,25	0,8	58	78	38	29	30	28
6151	C	A	HELD_MAL_ADR	0,87	1,15	58	76	40	58	83	33
6236	T	C	HELD_ALL_ADR	0,85	1,18	129	177	81	128	193	63
6277	T	G	HELD_FEM_ADR5ULN	0,44	2,25	16	21	11	66	112	20
6277	T	G	HELD_ALL_ADR5ULN	0,6	1,67	23	33	13	124	205	43
6277	T	G	HELD_FEM_ADR	0,73	1,37	72	105	39	66	112	20
6277	T	G	HELD_FEM_ADR3ULN	0,58	1,74	30	42	18	66	112	20
6313	C	T	HELD_FEM_UEFF	0,79	1,26	52	54	50	72	89	55
6369	T	C	HELD_FEM_LIP	1,31	0,77	63	82	44	68	72	64
6374	T	C	HELD_ALL_ADR3ULN	0,63	1,58	47	52	42	126	177	75
6374	T	C	HELD_MAL_ADR3ULN	0,47	2,13	17	15	19	58	79	37
6396	T	C	HELD_MAL_CC	0	null	14	0	28	18	30	6
6396	T	C	HELD_ALL_CC	1,76	0,57	45	83	7	40	65	15
6396	T	C	CVD_FEM	0,66	1,51	35	55	15	37	67	7
6396	T	C	CVD_ALL	0,77	1,3	97	167	27	70	130	10

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
6486	G	A	HELD_ALL_CC2	0,76	1,31	86	140	32	69	124	14
6520	G	A	HELD_MAL_ADR5ULN	0,52	1,92	8	11	5	60	99	21
6520	G	A	HELD_MAL_ADR3ULN	0,63	1,59	16	23	9	60	99	21
6520	G	A	HELD_ALL_ADR5ULN	0,61	1,63	25	35	15	131	212	50
6520	G	A	HELD_MAL_ADR	0,86	1,16	62	96	28	60	99	21
6522	G	A	HELD_FEM_ADR3ULN	0,75	1,33	31	49	13	71	121	21
6522	G	A	HELD_FEM_ADR	0,79	1,27	73	113	33	71	121	21
6524	A	G	HELD_MAL_ADR3ULN	2,36	0,42	17	26	8	59	62	56
6596	C	T	HELD_FEM_ADR3ULN	0,34	2,92	31	49	13	71	138	4
6596	C	T	HELD_FEM_ADR5ULN	0,26	3,89	17	27	7	71	138	4
6596	C	T	HELD_ALL_ADR3ULN	0,44	2,27	48	81	15	131	250	12
6596	C	T	HELD_FEM_ADR	0,58	1,72	73	127	19	71	138	4
6596	C	T	HELD_ALL_ADR5ULN	0,37	2,67	26	44	8	131	250	12
6596	C	T	HELD_ALL_ADR	0,72	1,38	136	246	26	131	250	12
6734	A	C	HELD_ALL_CC	0,41	2,43	12	21	3	15	30	0
6743	G	C	HELD_ALL_ADR	0,95	1,05	125	153	97	117	149	85
7128	C	T	HELD_ALL_ADR3ULN	2,09	0,48	44	75	13	114	157	71
7128	C	T	HELD_FEM_ADR3ULN	2,11	0,47	28	47	9	59	77	41
7128	C	T	HELD_ALL_ADR5ULN	2,22	0,45	23	39	7	114	157	71
7128	C	T	HELD_FEM_ADR	1,32	0,76	66	101	31	59	77	41
7128	C	T	HELD_FEM_ADR5ULN	2,25	0,44	15	25	5	59	77	41
7363	G	A	HELD_FEM_LIP	0,77	1,3	81	113	49	79	127	31

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
7363	G	A	HELD_ALL_LIP	0,78	1,28	100	143	57	115	185	45
7409	A	G	HELD_FEM_ADR5ULN	0,37	2,67	17	24	10	72	130	14
7409	A	G	HELD_FEM_ADR3ULN	0,54	1,85	31	48	14	72	130	14
7409	A	G	HELD_MAL_ADR5ULN	null	0	7	14	0	59	95	23
8138	T	C	HELD_MAL_LIP	2,16	0,46	19	28	10	35	33	37
8138	T	C	HELD_MAL_CC	1,25	0,8	14	16	12	19	18	20
8138	T	C	HELD_ALL_LIP	1,22	0,82	94	112	76	114	116	112
8168	C	A	HELD_MAL_LIP	0,48	2,1	19	28	10	36	66	6
8168	C	A	HELD_FEM_LIP	1,3	0,77	79	136	22	79	125	33
8210	G	A	HELD_ALL_ADR3ULN	0,95	1,05	46	53	39	124	147	101
8210	G	A	HELD_FEM_ADR3ULN	0,83	1,2	29	30	28	67	78	56
8210	G	A	HELD_FEM_ADR	0,86	1,16	69	70	68	67	78	56
8210	G	A	HELD_ALL_ADR	0,9	1,11	127	137	117	124	147	101
8241	A	G	HELD_FEM_LIP	1,66	0,6	76	136	16	77	120	34
8241	A	G	HELD_ALL_LIP	1,38	0,72	95	166	24	112	179	45
8249	C	T	HELD_ALL_ADR3ULN	0,57	1,75	48	86	10	129	246	12
8249	C	T	HELD_ALL_ADR5ULN	0,47	2,12	26	46	6	129	246	12
8480	C	G	CVD_FEM	0,38	2,63	27	48	6	39	78	0
8480	C	G	CVD_MAL	0,59	1,69	54	99	9	34	68	0
8577	T	C	HELD_ALL_ADR3ULN	0,68	1,48	47	50	44	126	167	85
8577	T	C	HELD_ALL_ADR	0,83	1,2	132	151	113	126	167	85
8577	T	C	HELD_ALL_ADR5ULN	0,61	1,63	26	27	25	126	167	85

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
8578	G	A	HELD_ALL_ADR3ULN	0,7	1,43	48	51	45	130	169	91
8653	C	T	HELD_MAL_ADR	2,22	0,45	47	87	7	52	81	23
8653	C	T	HELD_MAL_ADR3ULN	6	0,17	14	27	1	52	81	23
8653	C	T	HELD_MAL_ADR5ULN	null	0	7	14	0	52	81	23
8653	C	T	HELD_ALL_ADR3ULN	1,74	0,58	41	74	8	114	187	41
8816	G	C	HELD_FEM_LIP2	1,18	0,84	315	403	227	370	419	321
8816	G	C	HELD_FEM_HDL	1,9	0,53	18	24	12	22	17	27
8816	G	C	HELD_ALL_CC2	1,25	0,8	90	121	59	70	78	62
8816	G	C	CVD_ALL	0,78	1,28	92	138	46	65	111	19
8816	G	C	HELD_FEM_CC2	1,37	0,73	52	71	33	42	44	40
8816	G	C	HELD_MAL_HDL	0,99	1,01	18	22	14	17	21	13
8931	C	T	HELD_FEM_ADR3ULN	2,16	0,46	23	43	3	42	70	14
8943	A	C	HELD_MAL_ADR3ULN	3,52	0,28	16	30	2	55	85	25
9243	C	G	HELD_FEM_VEFF	1,17	0,85	139	230	48	143	223	63
9243	C	G	HELD_MAL_ADR5ULN	2,32	0,43	9	16	2	60	91	29
9243	C	G	HELD_FEM_UEFF	1,31	0,77	54	90	18	74	113	35
9523	G	A	HELD_MAL_ADR5ULN	0,37	2,69	8	12	4	60	109	11
9940	C	T	HELD_MAL_CC	null	0	12	24	0	14	23	5
9940	C	T	HELD_ALL_CC	2	0,5	38	71	5	31	50	12
10091	T	C	HELD_ALL_ADR3ULN	0,66	1,52	48	74	22	129	222	36
10541	G	C	HELD_FEM_UEFF	1,89	0,53	55	103	7	77	131	23
10541	G	C	HELD_FEM_VEFF	1,46	0,68	151	283	19	145	256	34

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
10600	G	A	CVD_MAL	0	null	67	0	134	34	64	4
10600	G	A	HELD_ALL_HDL	0	null	39	0	78	47	88	6
10600	G	A	HELD_MAL_HDL	0	null	19	0	38	23	42	4
10745	G	A	HELD_MAL_LIP	1,96	0,51	19	32	6	35	47	23
10748	T	C	HELD_MAL_LIP	0,53	1,89	13	15	11	30	47	13
10749	C	G	HELD_FEM_LIP	1,34	0,75	81	124	38	77	100	54
10785	T	C	CVD_MAL	1,47	0,68	69	128	10	33	55	11
10811	A	G	HELD_FEM_LIP2	1,18	0,85	243	382	104	300	440	160
10811	A	G	CVD_ALL	0,82	1,22	103	155	51	74	124	24
10830	G	A	HELD_ALL_LIP2	1,13	0,89	637	723	551	725	742	708
10830	G	A	HELD_ALL_LIP	1,35	0,74	99	113	85	114	98	130
10830	G	A	HELD_MAL_LIP2	1,16	0,86	314	357	271	347	346	348
10830	G	A	CVD_FEM	1,56	0,64	35	44	26	39	33	45
10830	G	A	HELD_MAL_LIP	1,84	0,54	19	24	14	36	29	43
10830	G	A	HELD_FEM_LIP	1,25	0,8	80	89	71	78	69	87
10949	G	C	HELD_FEM_VEFF	0,83	1,2	140	163	117	143	191	95
10949	G	C	HELD_FEM_EFF	0,88	1,14	269	319	219	282	369	195
10962	A	G	CVD_FEM	0,33	3,07	18	2	34	18	9	27
10962	A	G	HELD_ALL_ADR3ULN	1,27	0,79	47	75	19	117	173	61
10966	T	C	HELD_ALL_ADR3ULN	1,36	0,74	47	74	20	126	179	73
10966	T	C	HELD_ALL_ADR5ULN	1,92	0,52	25	42	8	126	179	73
11000	T	C	HELD_MAL_LIP2	1,19	0,84	313	483	143	348	495	201

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
11000	T	C	CVD_FEM	0,99	1,01	35	54	16	40	62	18
11000	T	C	HELD_MAL_ADR3ULN	0,53	1,9	17	18	16	60	87	33
11000	T	C	HELD_ALL_LIP2	1,11	0,9	630	973	287	725	1069	381
11000	T	C	HELD_MAL_ADR5ULN	0,44	2,29	9	9	9	60	87	33
11001	T	C	HELD_MAL_LIP2	1,19	0,84	309	476	142	333	471	195
11001	T	C	HELD_ALL_LIP2	1,12	0,89	620	960	280	709	1044	374
11001	T	C	CVD_FEM	1,01	0,99	34	52	16	40	61	19
11001	T	C	HELD_MAL_ADR3ULN	0,53	1,9	17	18	16	60	87	33
11001	T	C	HELD_ALL_LIP	1,28	0,78	102	163	41	115	165	65
11020	C	T	HELD_MAL_ADR3ULN	2,23	0,45	15	25	5	58	76	40
11073	G	C	HELD_FEM_LIP	0,79	1,27	79	90	68	78	107	49
11073	G	C	HELD_ALL_CC2	0,84	1,19	106	134	78	68	100	36
11192	T	A	HELD_FEM_ADR5ULN	0,7	1,42	16	20	12	70	101	39
11192	T	A	HELD_FEM_ADR3ULN	0,77	1,31	29	37	21	70	101	39
11248	C	T	HELD_FEM_ADR3ULN	1,94	0,52	30	51	9	68	95	41
11248	C	T	HELD_ALL_ADR	1,24	0,81	131	205	57	125	176	74
11410	G	T	HELD_FEM_VEFF	1,16	0,86	138	154	122	141	137	145
11448	G	A	HELD_MAL_HDL	0,41	2,43	19	21	17	25	45	5
11448	G	A	HELD_MAL_LIP	0,45	2,2	19	25	13	36	64	8
11448	G	A	HELD_MAL_LIP2	0,86	1,17	312	478	146	344	562	126
11448	G	A	HELD_ALL_LIP2	0,88	1,13	628	962	294	718	1157	279
11448	G	A	HELD_ALL_HDL	0,64	1,55	42	59	25	56	95	17

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
11448	G	A	HELD_FEM_ADR	0,73	1,38	69	99	39	68	114	22
11448	G	A	HELD_ALL_ADR	0,79	1,27	127	190	64	124	207	41
11448	G	A	HELD_ALL_CC	0,75	1,34	44	62	26	40	66	14
11450	T	A	HELD_MAL_LIP	0,42	2,37	19	21	17	36	61	11
11456	A	G	CVD_FEM	0,48	2,11	34	59	9	40	79	1
11462	G	T	HELD_MAL_LIP2	0,79	1,27	317	566	68	350	653	47
11462	G	T	HELD_ALL_LIP2	0,87	1,15	635	1142	128	735	1355	115
11483	T	C	HELD_FEM_ADR5ULN	0,41	2,41	17	30	4	69	133	5
11483	T	C	HELD_FEM_ADR3ULN	0,54	1,84	31	56	6	69	133	5
11483	T	C	HELD_FEM_ADR	0,73	1,36	73	135	11	69	133	5
11531	G	A	HELD_FEM_CC	0,64	1,56	31	47	15	22	41	3
11536	C	G	HELD_ALL_CC	0,95	1,06	43	66	20	40	63	17
11537	A	G	HELD_MAL_ADR	0,76	1,32	63	93	33	60	101	19
11558	A	C	HELD_MAL_LIP2	0,82	1,22	313	502	124	347	596	98
11558	A	C	HELD_ALL_LIP2	0,86	1,16	633	1036	230	722	1239	205
11558	A	C	HELD_ALL_CC	1,48	0,68	45	81	9	40	65	15
11585	G	T	HELD_MAL_CC	2,35	0,43	14	22	6	18	17	19
11594	T	C	HELD_ALL_ADR3ULN	5,88	0,17	46	91	1	127	234	20
11594	T	C	HELD_MAL_ADR	2,29	0,44	61	119	3	58	106	10
11614	T	C	HELD_FEM_CC	1,52	0,66	31	52	10	22	30	14
11614	T	C	HELD_MAL_CC2	1,49	0,67	48	84	12	29	43	15
11614	T	C	HELD_ALL_CC	1,24	0,8	45	74	16	40	60	20

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
11614	T	C	HELD_ALL_HDL	1,02	0,98	45	76	14	59	99	19
11631	G	A	HELD_MAL_ADR5ULN	0,35	2,9	9	8	10	59	87	31
11631	G	A	HELD_MAL_ADR3ULN	0,55	1,82	17	19	15	59	87	31
11637	A	C	HELD_FEM_LIP	0,77	1,29	77	101	53	79	121	37
11637	A	C	HELD_ALL_LIP	0,76	1,31	96	123	69	114	171	57
11637	A	C	CVD_MAL	1,32	0,76	69	111	27	34	45	23
11637	A	C	CVD_ALL	1,28	0,78	105	169	41	74	104	44
11641	G	C	HELD_MAL_ADR	1,22	0,82	60	74	46	57	59	55
11645	G	A	HELD_FEM_CC	2,45	0,41	31	60	2	22	38	6
11646	C	T	HELD_FEM_LIP	1,31	0,77	81	122	40	79	102	56
11646	C	T	HELD_ALL_LIP	1,27	0,79	100	150	50	115	152	78
11652	C	T	HELD_MAL_LIP	1,02	0,98	19	22	16	35	40	30
11727	G	A	HELD_ALL_ADR5ULN	0	null	20	0	40	104	170	38
11727	G	A	HELD_MAL_ADR3ULN	0	null	13	0	26	46	68	24
11727	G	A	HELD_MAL_ADR5ULN	0	null	8	0	16	46	68	24
11727	G	A	HELD_ALL_ADR3ULN	3,06	0,33	37	70	4	104	170	38
11727	G	A	HELD_FEM_ADR5ULN	0	null	12	0	24	58	102	14
11728	T	C	HELD_ALL_ADR5ULN	2,43	0,41	24	44	4	128	205	51
11914	A	T	HELD_MAL_ADR3ULN	0,47	2,12	15	10	20	56	63	49
11938	T	C	HELD_ALL_ADR3ULN	1,17	0,85	48	64	32	132	163	101
11938	T	C	HELD_ALL_ADR5ULN	1,06	0,94	26	33	19	132	163	101
11938	T	C	HELD_FEM_ADR3ULN	1,11	0,9	31	38	24	72	83	61

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
11950	G	A	HELD_MAL_ADR5ULN	0	null	8	0	16	55	78	32
11950	G	A	HELD_MAL_ADR3ULN	3	0,33	15	27	3	55	78	32
11950	G	A	HELD_MAL_ADR	1,16	0,86	55	84	26	55	78	32
11951	G	A	HELD_MAL_ADR5ULN	0	null	7	0	14	58	84	32
11951	G	A	HELD_FEM_UEFF	0,74	1,35	55	82	28	76	127	25
12008	C	T	HELD_ALL_ADR	1,95	0,51	119	234	4	113	215	11
12031	A	G	HELD_ALL_ADR3ULN	0,92	1,09	47	51	43	126	144	108
12031	A	G	HELD_FEM_ADR5ULN	0,55	1,81	17	13	21	70	79	61
12031	A	G	HELD_ALL_ADR5ULN	0,61	1,64	26	22	30	126	144	108
12031	A	G	HELD_FEM_ADR3ULN	0,8	1,25	30	29	31	70	79	61
12031	A	G	HELD_ALL_ADR	0,87	1,15	133	133	133	126	144	108
12031	A	G	HELD_FEM_ADR	0,83	1,2	72	68	76	70	79	61
12032	T	C	HELD_FEM_UEFF	0,56	1,78	51	88	14	71	136	6
12032	T	C	HELD_FEM_ADR	0,68	1,48	73	130	16	70	134	6
12032	T	C	HELD_ALL_ADR	0,75	1,34	134	240	28	128	242	14
12032	T	C	HELD_FEM_VEFF	0,78	1,28	136	243	29	140	262	18
12148	G	A	HELD_MAL_ADR5ULN	0,31	3,21	8	7	9	55	83	27
12148	G	A	HELD_MAL_ADR	0,71	1,4	55	66	44	55	83	27
12148	G	A	HELD_MAL_ADR3ULN	0,52	1,92	16	18	14	55	83	27
12207	A	G	HELD_MAL_ADR5ULN	0,79	1,26	9	12	6	58	84	32
12207	A	G	HELD_MAL_ADR	0,81	1,24	59	74	44	58	84	32
12207	A	G	HELD_MAL_ADR3ULN	0,84	1,19	17	23	11	58	84	32

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
12399	A	G	HELD_MAL_ADR5ULN	0,36	2,8	8	11	5	60	106	14
12399	A	G	HELD_MAL_ADR3ULN	0,51	1,97	16	24	8	60	106	14
12399	A	G	HELD_ALL_ADR	0,79	1,26	132	217	47	131	232	30
12554	A	T	HELD_MAL_ADR	0,71	1,41	62	98	26	55	99	11
12554	A	T	HELD_FEM_VEFF	0,82	1,23	151	234	68	144	243	45
12851	T	C	HELD_FEM_ADR5ULN	0,52	1,92	17	22	12	71	115	27
12851	T	C	HELD_MAL_ADR	1,07	0,94	62	94	30	60	88	32
13025	A	C	HELD_MAL_ADR3ULN	1,06	0,94	17	24	10	58	80	36
13025	A	C	HELD_FEM_ADR5ULN	0,7	1,43	17	19	15	70	93	47
13191	G	A	HELD_ALL_CC	0,72	1,39	43	50	36	39	58	20
13192	T	C	HELD_MAL_ADR3ULN	0,68	1,46	17	25	9	59	97	21
13192	T	C	HELD_MAL_ADR5ULN	0,79	1,27	9	14	4	59	97	21
13192	T	C	HELD_ALL_ADR3ULN	0,99	1,01	47	77	17	129	212	46
13192	T	C	HELD_MAL_ADR	0,94	1,06	61	98	24	59	97	21
13193	G	A	HELD_MAL_ADR3ULN	0,68	1,48	16	23	9	58	94	22
13193	G	A	HELD_MAL_ADR5ULN	0,74	1,36	8	12	4	58	94	22
13193	G	A	HELD_ALL_ADR3ULN	1,02	0,98	47	77	17	130	212	48
13338	G	A	HELD_FEM_UEFF	1,09	0,92	55	75	35	71	92	50
13338	G	A	HELD_FEM_VEFF	0,98	1,02	148	187	109	139	178	100
13339	G	A	HELD_MAL_ADR	0,9	1,11	50	42	58	50	47	53
13339	G	A	CVD_FEM	1,92	0,52	31	57	5	35	56	14
13340	C	A	HELD_FEM_VEFF	0,58	1,71	21	21	21	17	27	7

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
13479	G	A	HELD_FEM_UEFF	0,68	1,47	48	73	23	65	113	17
13633	T	C	HELD_FEM_ADR3ULN	0,59	1,68	27	36	18	69	112	26
13633	T	C	HELD_FEM_ADR	0,75	1,33	64	90	38	69	112	26
13929	G	A	HELD_MAL_ADR5ULN	0	null	8	0	16	54	94	14
14065	C	T	HELD_FEM_EFF	0,81	1,23	267	473	61	271	501	41
14083	T	C	HELD_FEM_ADR	1,5	0,67	69	123	15	70	112	28
14085	T	C	HELD_FEM_EFF	0,87	1,14	240	405	75	230	404	56
14087	T	C	HELD_FEM_EFF	0,87	1,14	268	452	84	283	496	70
14102	C	T	HELD_MAL_ADR5ULN	1,1	0,91	9	12	6	56	72	40
14102	C	T	HELD_FEM_EFF	1,15	0,87	271	361	181	281	340	222
14103	C	T	HELD_FEM_EFF	0,85	1,18	264	445	83	273	482	64
14103	C	T	HELD_FEM_VEFF	0,92	1,09	137	234	40	135	236	34
14103	C	T	HELD_FEM_UEFF	0,73	1,38	53	84	22	69	121	17
14129	A	G	HELD_ALL_ADR3ULN	0,77	1,29	47	53	41	116	151	81
14129	A	G	HELD_MAL_ADR3ULN	0,74	1,35	16	18	14	55	72	38
14326	A	C	HELD_FEM_EFF	1,18	0,85	272	454	90	285	449	121
14503	C	T	HELD_ALL_ADR5ULN	1,14	0,88	24	34	14	114	154	74
14503	C	T	HELD_ALL_ADR3ULN	0,91	1,1	45	58	32	114	154	74
14503	C	T	HELD_FEM_ADR5ULN	0,99	1,01	16	21	11	57	75	39
14503	C	T	HELD_FEM_ADR3ULN	0,86	1,17	29	35	23	57	75	39
14537	C	T	HELD_ALL_ADR	0,77	1,29	118	133	103	113	156	70
14537	C	T	HELD_FEM_ADR	0,77	1,29	67	68	66	59	76	42

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
15915	T	C	HELD_FEM_ADR	1,07	0,94	63	95	31	55	80	30
15915	T	C	HELD_ALL_ADR	1,08	0,92	111	172	50	106	158	54
15915	T	C	HELD_ALL_ADR3ULN	1,89	0,53	38	66	10	106	158	54
19289	G	A	HELD_MAL_CC	0,56	1,8	12	20	4	18	34	2
19289	G	A	HELD_ALL_CC	0,72	1,38	43	71	15	40	73	7
19289	G	A	HELD_MAL_LIP	0,57	1,75	19	27	11	34	59	9
36958	C	G	HELD_MAL_ADR3ULN	null	0	15	30	0	57	104	10
37158	C	A	HELD_ALL_ADR	0,79	1,27	122	139	105	114	157	71
37158	C	A	HELD_FEM_ADR	0,78	1,29	66	70	62	58	77	39
37160	C	T	HELD_FEM_UEFF	0,65	1,54	53	86	20	73	133	13
37412	T	G	HELD_FEM_ADR5ULN	0,6	1,68	17	19	15	69	98	40
37412	T	G	HELD_ALL_ADR5ULN	0,69	1,46	26	32	20	129	185	73
37412	T	G	HELD_FEM_ADR3ULN	0,65	1,53	31	35	27	69	98	40
37457	T	A	CVD_ALL	2,53	0,4	53	101	5	28	43	13
37457	T	A	CVD_FEM	5,5	0,18	17	33	1	18	27	9
37457	T	A	CVD_MAL	1,62	0,62	36	68	4	10	16	4
37704	C	T	HELD_MAL_ADR5ULN	0,12	8,06	9	17	1	60	120	0
38959	C	A	CVD_ALL	0,94	1,06	57	99	15	31	55	7
38959	C	A	HELD_FEM_EFF	1,2	0,83	282	526	38	280	508	52
39292	G	A	HELD_FEM_ADR5ULN	0,38	2,61	9	12	6	47	82	12
39292	G	A	HELD_ALL_ADR5ULN	0,49	2,04	17	26	8	86	153	19
39698	T	C	HELD_MAL_ADR3ULN	0,67	1,5	16	13	19	56	60	52

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
39756	T	C	HELD_FEM_ADR3ULN	1,85	0,54	19	29	9	44	51	37
39951	T	C	HELD_MAL_ADR	1,24	0,81	52	78	26	54	72	36
39951	T	C	HELD_ALL_ADR	0,96	1,04	117	161	73	113	159	67
39951	T	C	HELD_FEM_ADR	0,81	1,23	65	83	47	59	87	31
39951	T	C	HELD_FEM_ADR5ULN	0,5	2,01	14	15	13	59	87	31
40466	G	T	HELD_FEM_EFF	1,31	0,76	266	469	63	266	436	96
40466	G	T	HELD_FEM_UEFF	1,62	0,62	52	93	11	69	110	28
40466	G	T	HELD_FEM_VEFF	1,32	0,76	139	244	34	135	219	51
44442	A	G	HELD_MAL_ADR5ULN	0,41	2,45	9	8	10	59	82	36
55504	T	C	HELD_MAL_ADR	1,33	0,75	60	75	45	56	54	58
55542	C	A	HELD_FEM_ADR	0,75	1,33	65	62	68	69	85	53
55670	C	T	HELD_FEM_VEFF	1,62	0,62	154	297	11	138	254	22
55736	A	G	HELD_ALL_ADR5ULN	null	0	15	30	0	87	147	27
55736	A	G	HELD_MAL_ADR5ULN	null	0	7	14	0	43	71	15
55736	A	G	HELD_FEM_ADR5ULN	null	0	8	16	0	44	76	12
55748	T	C	HELD_MAL_ADR5ULN	0	null	8	0	16	56	98	14
55813	T	C	HELD_ALL_ADR3ULN	0,66	1,51	44	39	49	119	139	99
55845	C	A	HELD_FEM_VEFF	0,81	1,24	136	152	120	135	179	91
55845	C	A	HELD_MAL_ADR3ULN	2,11	0,47	16	25	7	58	68	48
55845	C	A	HELD_FEM_UEFF	0,74	1,35	52	58	46	68	93	43
55923	C	T	HELD_FEM_ADR	0,74	1,35	59	63	55	57	78	36
55923	C	T	HELD_FEM_ADR3ULN	0,6	1,67	27	27	27	57	78	36

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
55945	G	A	HELD_FEM_ADR	0,7	1,43	66	70	62	65	92	38
55945	G	A	HELD_FEM_ADR3ULN	0,58	1,73	28	29	27	65	92	38
55945	G	A	HELD_ALL_ADR	0,82	1,22	124	142	106	122	163	81
56007	T	C	HELD_MAL_ADR3ULN	1,57	0,64	17	26	8	49	63	35
56007	T	C	HELD_MAL_ADR5ULN	1,77	0,56	9	14	4	49	63	35
56011	A	G	HELD_ALL_ADR5ULN	null	0	24	48	0	120	228	12
56104	G	A	HELD_FEM_UEFF	0,71	1,41	56	62	50	76	106	46
56113	G	T	HELD_ALL_ADR5ULN	0,57	1,74	24	20	28	114	133	95
56113	G	T	HELD_ALL_ADR3ULN	0,84	1,19	45	47	43	114	133	95
56113	G	T	HELD_FEM_ADR5ULN	0,53	1,9	17	13	21	58	68	48
56113	G	T	HELD_FEM_ADR3ULN	0,73	1,37	30	28	32	58	68	48
56636	T	C	HELD_FEM_ADR	0,94	1,07	70	72	68	59	65	53
56636	T	C	HELD_FEM_ADR3ULN	1,08	0,92	31	36	26	59	65	53
56636	T	C	HELD_FEM_ADR5ULN	0,93	1,07	18	19	17	59	65	53
56666	G	A	HELD_MAL_ADR3ULN	0	null	13	0	26	55	89	21
56666	G	A	HELD_MAL_ADR5ULN	0	null	8	0	16	55	89	21
56666	G	A	HELD_MAL_ADR	1,86	0,54	51	94	8	55	89	21
56667	T	C	HELD_FEM_EFF	1,17	0,85	264	342	186	265	304	226
56667	T	C	HELD_MAL_ADR3ULN	2,22	0,45	17	28	6	56	71	41
56667	T	C	HELD_FEM_ADR3ULN	0,66	1,52	30	29	31	67	85	49
56780	G	A	HELD_FEM_ADR3ULN	0,56	1,78	26	19	33	50	58	42
56780	G	A	HELD_FEM_ADR	0,74	1,36	62	51	73	50	58	42

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
56780	G	A	HELD_ALL_ADR3ULN	0,61	1,65	36	28	44	94	105	83
56780	G	A	HELD_ALL_ADR	0,83	1,21	105	96	114	94	105	83
56876	T	C	HELD_FEM_UEFF	1,91	0,52	57	106	8	74	123	25
56876	T	C	HELD_FEM_EFF	1,29	0,77	285	524	46	274	480	68
56876	T	C	HELD_FEM_VEFF	1,42	0,71	154	285	23	143	248	38
56978	A	G	HELD_ALL_ADR5ULN	2,13	0,47	26	42	10	124	157	91
57000	A	T	HELD_FEM_VEFF	0,93	1,08	150	206	94	143	206	80
57000	A	T	HELD_FEM_UEFF	1,03	0,97	54	76	32	75	104	46
57000	A	T	CVD_ALL	1,3	0,77	57	91	23	32	43	21
57000	A	T	CVD_MAL	1,23	0,82	39	64	14	13	18	8
57313	T	C	HELD_FEM_UEFF	0,79	1,26	55	65	45	76	104	48
57734	C	G	HELD_FEM_ADR3ULN	0,61	1,63	30	45	15	67	116	18
57837	A	G	HELD_MAL_ADR3ULN	3,15	0,32	15	28	2	53	83	23
57853	T	C	HELD_FEM_EFF	1,26	0,79	265	457	73	265	425	105
57853	T	C	HELD_FEM_UEFF	1,62	0,62	52	91	13	68	104	32
57853	T	C	HELD_FEM_VEFF	1,26	0,79	139	238	40	135	214	56
57854	G	A	HELD_FEM_EFF	1,17	0,86	267	451	83	262	420	104
57854	G	A	HELD_FEM_UEFF	1,52	0,66	52	90	14	68	104	32
57854	G	A	HELD_MAL_ADR3ULN	2,61	0,38	16	29	3	57	86	28
58295	A	G	HELD_MAL_ADR	0,78	1,29	56	48	64	54	60	48
58402	T	C	HELD_MAL_ADR3ULN	0,49	2,04	17	10	24	56	57	55
58407	G	T	HELD_FEM_VEFF	1,04	0,97	153	195	111	145	180	110

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
58407	G	T	HELD_FEM_UEFF	1,23	0,82	56	76	36	76	91	61
58440	T	C	HELD_FEM_UEFF	0,68	1,48	52	81	23	72	127	17
58525	C	T	HELD_FEM_ADR	0,55	1,83	66	110	22	66	128	4
58525	C	T	HELD_FEM_ADR3ULN	0,38	2,65	30	49	11	66	128	4
58525	C	T	HELD_FEM_ADR5ULN	0,28	3,55	16	26	6	66	128	4
58525	C	T	HELD_ALL_ADR	0,7	1,44	124	212	36	122	228	16
58525	C	T	HELD_ALL_ADR5ULN	0,47	2,14	25	42	8	122	228	16
58525	C	T	HELD_ALL_ADR3ULN	0,56	1,8	47	80	14	122	228	16
58533	C	T	HELD_FEM_ADR	0,59	1,69	67	114	20	71	136	6
58533	C	T	HELD_FEM_ADR3ULN	0,44	2,26	27	46	8	71	136	6
58533	C	T	HELD_FEM_ADR5ULN	0,38	2,67	14	24	4	71	136	6
58533	C	T	HELD_ALL_ADR	0,77	1,31	125	217	33	129	238	20
58544	G	A	HELD_MAL_ADR5ULN	0	null	6	0	12	54	85	23
58716	T	C	HELD_MAL_ADR3ULN	6,23	0,16	16	30	2	59	76	42
58716	T	C	HELD_MAL_ADR5ULN	3,42	0,29	8	14	2	59	76	42
58736	C	T	HELD_FEM_EFF	1,17	0,85	289	395	183	281	344	218
58808	A	G	HELD_FEM_ADR	1,34	0,75	68	100	36	61	74	48
58809	C	A	HELD_MAL_ADR5ULN	0	null	9	0	18	59	96	22
58809	C	A	HELD_ALL_ADR3ULN	0,7	1,42	46	70	22	128	215	41
58809	C	A	HELD_MAL_ADR3ULN	0,67	1,5	16	23	9	59	96	22
58809	C	A	HELD_FEM_UEFF	1,53	0,65	54	94	14	75	116	34
58886	A	G	HELD_FEM_ADR3ULN	0,57	1,76	31	20	42	72	74	70

BAYSNP	ALLELE1	ALLELE2	COMPARISON_A	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
58886	A	G	HELD_ALL_ADR3ULN	0,66	1,53	48	38	58	132	142	122
58886	A	G	HELD_ALL_ADR5ULN	0,59	1,68	26	20	32	132	142	122
58926	C	T	HELD_MAL_ADR3ULN	0,39	2,56	15	12	18	54	75	33
58926	C	T	HELD_ALL_ADR5ULN	0,5	2	22	19	25	113	144	82
58926	C	T	CVD_FEM	1,07	0,94	18	21	15	19	21	17
58926	C	T	HELD_MAL_ADR5ULN	0,4	2,51	8	7	9	54	75	33
58968	A	G	HELD_ALL_ADR5ULN	0,44	2,27	22	21	23	118	168	68
58968	A	G	HELD_MAL_ADR3ULN	0,4	2,52	13	12	14	55	81	29
58968	A	G	HELD_ALL_ADR3ULN	0,64	1,55	41	47	35	118	168	68
58968	A	G	HELD_FEM_ADR5ULN	0,47	2,14	14	13	15	63	87	39
58985	G	A	HELD_ALL_ADR5ULN	0,52	1,93	26	28	24	130	188	72
59113	C	G	HELD_MAL_ADR5ULN	0,13	7,7	8	2	14	55	64	46
59113	C	G	HELD_MAL_ADR3ULN	0,42	2,39	16	10	22	55	64	46
59236	G	A	HELD_ALL_ADR	0,83	1,21	95	103	87	96	122	70
59236	G	A	HELD_ALL_ADR3ULN	0,83	1,21	34	39	29	96	122	70
59236	G	A	HELD_FEM_ADR	0,78	1,29	52	47	57	51	59	43
59237	C	T	HELD_FEM_VEFF	1	1	121	140	102	119	138	100
59237	C	T	HELD_FEM_EFF	1,04	0,96	240	290	190	243	285	201
59267	T	C	HELD_FEM_UEFF	0,64	1,55	50	52	48	68	96	40
59352	T	C	HELD_MAL_ADR	0,94	1,07	58	73	43	56	74	38
59352	T	C	HELD_ALL_ADR	1,01	0,99	126	167	85	125	164	86
59363	T	C	CVD_MAL	1,27	0,79	60	84	36	28	30	26

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
59368	T	C	HELD_FEM_ADR	0,7	1,42	66	74	58	69	100	38
59371	C	T	HELD_FEM_VEFF	0,89	1,13	141	153	129	136	164	108
59371	C	T	HELD_FEM_UEFF	0,85	1,18	52	60	44	68	88	48
59372	C	T	HELD_MAL_ADR	0,69	1,44	55	87	23	58	104	12
59372	C	T	HELD_MAL_ADR3ULN	0,5	2	17	26	8	58	104	12
59443	T	C	HELD_ALL_ADR5ULN	1,32	0,75	19	25	13	95	110	80
59443	T	C	HELD_MAL_ADR5ULN	0,93	1,08	7	7	7	45	47	43
900080	G	C	HELD_FEM_ADR3ULN	0,47	2,12	31	52	10	71	135	7
900080	G	C	HELD_FEM_ADR5ULN	0,42	2,36	17	29	5	71	135	7
900102	T	G	HELD_FEM_UEFF	1,55	0,65	55	73	37	78	76	80
900102	T	G	HELD_FEM_VEFF	1,23	0,82	153	204	102	147	168	126
900111	G	A	HELD_FEM_UEFF	1,48	0,68	55	73	37	78	79	77
900111	G	A	HELD_FEM_VEFF	1,2	0,83	151	198	104	146	166	126
900117	T	G	HELD_MAL_LIP	3,44	0,29	17	31	3	33	44	22
900118	G	A	HELD_FEM_EFF	1,6	0,63	252	469	35	259	444	74
900118	G	A	HELD_FEM_VEFF	1,47	0,68	130	241	19	130	225	35
900118	G	A	HELD_FEM_ADR5ULN	1,12	0,89	15	28	2	59	109	9
900118	G	A	HELD_ALL_ADR5ULN	0,81	1,24	23	42	4	110	205	15
900120	T	C	HELD_FEM_EFF	1,28	0,78	286	511	61	280	471	89
900121	T	G	HELD_FEM_EFF	0,88	1,13	269	353	185	266	379	153
900123	A	G	HELD_ALL_ADR	null	0	119	238	0	115	226	4
900123	A	G	HELD_FEM_ADR	null	0	64	128	0	59	115	3

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
900124	G	A	HELD_FEM_EFF	0,89	1,13	249	254	244	253	288	218
900132	T	C	HELD_FEM_ADR	1,21	0,83	67	111	23	58	89	27
900144	A	G	CVD_FEM	null	0	28	56	0	40	74	6
900144	A	G	HELD_ALL_ADR5ULN	null	0	26	52	0	125	240	10
900145	G	T	CVD_FEM	1,55	0,65	30	58	2	39	73	5
900145	G	T	HELD_ALL_ADR5ULN	null	0	25	50	0	121	232	10
900146	A	G	HELD_FEM_ADR5ULN	0,52	1,93	17	22	12	67	109	25
900146	A	G	HELD_FEM_CC	1,19	0,84	30	50	10	22	34	10
900146	A	G	HELD_MAL_ADR	1,21	0,82	58	97	19	54	84	24
900147	T	C	HELD_ALL_ADR3ULN	1,83	0,55	44	74	14	119	168	70
900147	T	C	HELD_FEM_ADR3ULN	2,12	0,47	28	48	8	66	91	41
900196	C	T	HELD_MAL_LIP	0,48	2,08	19	17	21	32	47	17
900196	C	T	HELD_FEM_LIP	2,71	0,37	12	19	5	36	37	35
900196	C	T	HELD_FEM_ADR3ULN	2,02	0,5	23	37	9	62	77	47
900196	C	T	CVD_FEM	1	1	6	8	4	15	20	10
900196	C	T	CVD_ALL	1,44	0,69	21	30	12	31	36	26
900200	T	C	CVD_FEM	0,58	1,71	20	23	17	38	58	18
900204	C	G	HELD_FEM_EFF	1,19	0,84	270	430	110	261	384	138
900205	C	G	HELD_FEM_EFF	0,9	1,12	283	364	202	274	380	168
900205	C	G	CVD_MAL	0,82	1,22	69	90	48	31	49	13
900223	G	A	HELD_FEM_ADR	3,59	0,28	43	85	1	31	57	5
900225	G	A	HELD_ALL_ADR5ULN	0	null	23	0	46	126	234	18

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
900225	G	A	HELD_MAL_ADR3ULN	0	null	15	0	30	57	104	10
900227	A	C	HELD_FEM_ADR5ULN	5,9	0,17	17	33	1	72	118	26
900233	T	A	HELD_FEM_ADR5ULN	1,39	0,72	17	23	11	72	84	60
900236	C	T	HELD_FEM_ADR3ULN	0,6	1,68	31	50	12	69	125	13
900236	C	T	HELD_MAL_ADR5ULN	null	0	9	18	0	60	104	16
900241	C	G	HELD_FEM_EFF	0,97	1,03	276	367	185	275	373	177
900242	G	C	HELD_ALL_ADR5ULN	0	null	26	0	52	132	220	44
900242	G	C	HELD_ALL_ADR3ULN	4,65	0,21	48	93	3	132	220	44
900242	G	C	HELD_FEM_ADR5ULN	0	null	17	0	34	72	119	25
900242	G	C	HELD_MAL_ADR3ULN	0	null	17	0	34	60	101	19
900242	G	C	HELD_FEM_ADR	1,87	0,54	73	136	10	72	119	25
900242	G	C	HELD_FEM_ADR3ULN	3,09	0,32	31	59	3	72	119	25
900242	G	C	HELD_ALL_ADR	1,42	0,7	136	246	26	132	220	44
900242	G	C	HELD_MAL_ADR5ULN	0	null	9	0	18	60	101	19